SEARCH REQUEST FORM

Scientific and Technical Information Center

tequester's Full Name:			#:		
un Unit: Phone 1	Number 30	Seria	Number:		
Mail Box and Bldg/Room Location	n:	Results Format	Preferred (circle):	PAPER	DISK E-MAIL
more than one search is subm	nitted, please pri	ioritize searche:	s in order of ne	ed.	

nclude the elected species or structures, I tility of the invention. Define any terms nown. Please attach a copy of the cover	keywords, synonyms s that may have a spe	, acronyms, and regical meaning. Give	istry numbers, and c	ombine wit	h the concept or
Title of Invention:			·		
nventors (please provide full names):		· · · · · · · · · · · · · · · · · · ·			
			<u> </u>		
Earliest Priority Filing Date:					
For Sequence Searches Only Please incli appropriate serial number.	ude all pertinent inforn	nation (parent, child,	divisional, or issued p	alent numbe	ers) along with the
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STAFF USE ONLY 0	Type of Searcl	h	Vendors and cost	where appl	licable
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Searcher Phone #: 308-450/	AA Sequence (#)_	Dialog	-		
Searcher Location: Best Like	Structure (#)	Questel/0	Orbit		
Date Searcher Picked Up: 8/31/0/	Bibliographic			, <u>-</u>	
Date Completed: 9/9/0/	Litigation	Lexis/Ne	xisABSS	0/	
Searcher Prep & Review Time:	Fulltext	Sequence	aystems _//kur		•

PTO-1590 (1-2000)

STIC-Biotech/ChemLib

From: Sent:

Jiang, Dong Thursday, August 30, 2001 6:15 PM STIC-Biotech/ChemLib

To:

Subject:

SN09/333,159

G/14/99 Mc Caxting

Please search SEQ ID NO:47 (back translation only)

-issued

-commercial

Please send results on paper to Dong Jiang in 10B-01 (mail stop CM1-10C01). Thank you very much for your help.

Dong Jiang (78243) 703-305-1345 U.S. Patent and Trademark Office Art Unit 1646 dong.jiang@uspto.gov CM1-10B01 Mail stop: CM1-10C01

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AC008342 Drosophila mele
AC017903 Drosophila mele
AE003811 Drosophila mele
AC013100 Drosophila melar
      AC004766 Drosophila melar
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LPDHLIKDLFGDKEFLPQSAFLKWLGTHVCTHVILKELCGNLCFLLCGFNERNLNMSR
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VPTAVWSGGHDWLADVYDVNILLTQITNLVFHESIPEWĘHLDFIWGLDAPWRLYNKII
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2626)
Ameis,D., Merkel,M., Eckerskorn,C. and Greten,H.
Purification, characterization and molecular cloning of human hepatic lysosomal acid lipase
Eur. J. Blochem. 219 (3), 905-914 (1994)
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FRG
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Submitted (29-NOV-1993) D. Ameis, Medical Department,
Hospital Eppendorf, Martinistrasse 52, 20246 Hamburg,
Location/Qualifiers
1. 2626
/organism="Homo sapiens"
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93932
175007
211784
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2.6e-44
3.3e-44
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146. .1345
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Ratio: 3.836
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LOCUS HSLAL
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gb_in1:AC004766
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gb_htg4:AC013100
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REFERENCE
AUTHORS
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VERSION
KEYWORDS
SOURCE
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AUTHORS
TITLE
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AR092632 Sequence 1 from pater
126319 Bos taurus pregastric
A39301 Sequence 2 from Patent
A39303 Sequence 4 from Patent
A39305 Sequence 6 from Patent
A39300 Sequence 1 from Patent
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AR092634 Sequence 4 from paten
AR039024 Sequence 6 from paten
AR092635 Sequence 6 from paten
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A01046 H.sapiens mRNA for huma
A12714 Pregastric lipase. 8/19
A57758 Sequence 3 from Patent
AX068259 Sequence 21 from Pate
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AC015461 Homo sapiens clone
AC011277 Homo sapiens clone
AL353113 Homo sapiens chromc
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! ACO84473 Caenorhabditis brigg
! U64849 Caenorhabditis elegans
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A57756 Sequence 1 from Patent
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-Os-Cap10_1/U28TO_2800-1/U3933159/runat_31082001_122330_1384/app_query.fasta_1.488
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-NORM-ext -MINIEN-0 -MAXLEN-200000000
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                                                                                                                           About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
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OM of: US-09-333-159-47 to: GenEmbl:*
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Ouery: US-09-333-159-47
Ouery length: 423
Database: GenEmbl:*
Database sequences: 1344157
Database length: -856060004
Search time (sec): 1547.640000
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gb_pri0.HSUNG464
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9b_in3:CELK04A8
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gb_patl:AR039023
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gb_pat2:AX068249
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Jb_pat1:A01046
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    250 ArgPheLeuArgGlnLeuValIleTyrLeuCysGlyGlnValIleLeuAs 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        857 GCGTTTTTGAAGTGGCTGGGTACCCACGTTTGCACTCATGTCATACTGAA 906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pGlnIleCysSerAsnIleMetLeuLeuGlyGlyPheAsnThrAsnA 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66
                                                                                                                                                                                           18 pLeuLeuIleLeuValAlaTyrMetPheGlnArgAsnValAsnSerValH 35
                                                                                                                      2 LeuGluThrLeuSerArgGlnTrplleValSerHisArgMetGluMetTr 18
                                                                                                                                                                                                               :::||| ||||||::: :::|||
157 GTTCTTGGGGTTGGTGTTCTGTTGTTCTGGACCCTGCATTCTGAGG
                                                                                                                                                                                                                                                            35 isMetProThrLys.....AlaValAspProGluAlaPheMetAsnIle
                                                                                                                                                                                                                                                                                                                                SerGluIleIleGlnHisGlnGlyTyrProCysGluGluTyrGluValAl
                                                                                                                                                                                                                                                                                                                                                                                                 66 aThrGluAspGlyTyrIleLeuSerValAsnArgIleProArgGlyLeuV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83 alGlnProLysLysThrGlySerArgProValValLeuLeuGlnH1sGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     757 TTCCGTCGCCTTCTGTACTAGCCCTATGGCCAAATTAGGACGATTACCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    807 ATCATCTCATTAAGGACTTATTTGGAGACAAAGAATTTCTTCCCCAGAGT
   Percent Identity: 60.732
                                                                                      from: 1
 83.171
                                                                                      to: HSLAL
                                                    US-09-333-159-47 x HSLAL
Percent Similarity:
                                alignment_block
                                                                                      Align seg 1/1
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Euküryöte, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2493)
Anderson, R.A. and Sando, G.N. Cloning and expression of cDNA encoding human lysosomal acid lipase/cholesteryl ester hydrolase. Similarities to gastric and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_blbck:
LOCUS HUMI<u>IPC</u>ML 2493 bp mRNA PRI 07-JAN-1995
<u>DEFINITION HUM</u>AIN lysosomal acid lipase/cholesteryl esterase mRNA, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="GDB:G00-120-153"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCAGAGTTATCCTCCCACATACAATGTGAAGGACATGCTTGTGCCGACT 1156
                                                                                                                                                                                                                                                                                                                                                                                                                                            349
                                                                                                                                                                                                                                                                                                                                         300 ThrSerValGlnAsnIleLeuHisTrpSerGlnAlaValAsnSerGlyGl 316
                                                                                                                                                                                         316 uLeuArqAlaPheAspTrpGlySerGluThrLysAsnLeuGluLysCysA 333
                                                                                                                                                                                                                                                                                                                                                                                                                      366 sMetLeuLeuSerGluValThrAsnLeuIleTyrHisLysAsnIleProG 383
907 GGAGCTCTGTGGAAATCTCTGTTTTTTGTGTGGATTTAATGAGAGAA
                                                                                                                                                                                                                                                                    snGlnP::OThrProValArgTyrArgValArgAspMetThrValProThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note-"alternate initiator ATG may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lysosomal acid lipase/cholesteryl esterase.
Homo sapiens fibroblast cDNA to mRNA.
Homo sapiens
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J. Biol. Chem. 266 (33), 22479-22484 (1991)
92042192
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1. .2493
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/db_xref="taxon:9606"
/tissue_type="fibroblast"
/map="10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1307 TATAATAAATTATTAATCTAATGAGGAAA 1336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TyrAsnGluIleIleHisLeuMetGlnGln 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /EC_number="3.1.1.13'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="LIPA"
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M74775.1 GI:187151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_hame: sb_pr:: HUMLIPCHL
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VERSION
KEYWORDS
SOURCE
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AUTHORS
TITLE
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MEDLINE
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GAGGAANTACCTGGTCTCGGAAACATAAGACACTCTCAGTTTCTCAGGAT
                                       150 GluPheTrpAlaPheSerTyrAspGluMetAlaArgPheAspLeuProAl
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                                                                        NKTGOEQVYYVGHSQGTTIGFIAFSQIPELAKRIKMFFALGPVASVAFCTSPMAKLGR
PEHLINDERFEDERELPQSAFLKWLGGTHVCTHVILKELCGNLCFLLCGFNERNLMSR
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                                                                                                                                                                                                                                                                                                                                                         /product-"lysosomal acid lipase/cholesteryl esterase"
2466. 2471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  352 GGGCTTCATTCTTGCTGATGCTGTTTTGACGTGTGGGATGGGCAACAGCA 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SerGluileileGlnHisGlnGlyTyrProCysGluGluTyrGluValAl 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 aThrGluAspGlyTyrIleLeuSerValAsnArgIleProArgGlyLeuV 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35 IsMetProThrLys.....AlaValAspProGluAlaPheMetAsnIle 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 LeuGluThrLeuSerArgGlnTrpIleValSerHisArgMetGluMetTr 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 CTCGAGACAGCGGCCCGGCAG.....GACAGCTCCAGAATGAAAATGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83 alGlnProLysLysThrGlySerArgProValValLeuLeuGlnHisGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              202 GACAGAAGATGGATATTTCTGTGCCTTAACCGAATTCCTCATGGGAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       252 AGAACCATTCTGACAAAGTCCCAAACCAGTTGTTCTTCCTGCAACATGGC
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Percent Identity: 60.732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to: 2493
                                                                                                                                                                                                                                                                                           /gene="LIPA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                       2493
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/note="GO0-120-153"
'44 c 516 g
_xref="GI:187152"
                                                                                                                                                                                                                                                                                                                                                                                                                  /note="G00-120-153"
2493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: HUMLIPCHL from: 1
                                                                                                                                                                         41. .103
/gene="LIPA"
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US-09-333-159-47 x HUMLIPCHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality: 1306.00
Ratio: 3.841
Milarity: 82.927
                                                                                                                                                          NLMRKYO
                                                                                                                                                                                                                                                                                                                                                                                              /gene-
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HSLYACLY 2481 bp mRNA PRI 17-
H.Sapiens (HepG2) LAL mRNA for lysosomal acid lipase.
231690
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                901
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                383 luTrpAlaHisValAspPheIleTrpGlyLeuAspAlaProHisArgMet 399
               501
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                                                aValllaAsnPhelleLeuGlnLysThrGlyGlnGluLysIleTyrTyrV
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                                                                                                                                                                                                                                                                                                 spMetMetIleLysGlyLeuPheGlyLysLysGluPheLeuTyrGlnThr
                                                                                                                                                                                                                                                                                                                                                                         266 pGlnIlaCysSerAsnIleMetLeuLeuLeuGlyGlyPheAsnThrAsnA
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502 IICCATITAACIICTGAAIAAACIGGCCAAGAACAAGIGIAIIAIG
                                                                                                                                              ProGluceualaGlnLysIteLysMetTyrPhealaLeualaProIleal
                                                                                                                                                                                                                                       602 CCTGAGGTGCTAAAAGGATTAAAATGTTTTTTGCCCTGGGTCCTGTGGC
                                                                                                                                                                                                                                                                            aThrvalLysHisAlaLysSerProGlyThrLysPheLeuLeuLeuProA
                                                                                                                                                                                                                                                                                                                                                                                                                           250 ArgPheLeuArgGlnLeuValIleTyrLeuCysGlyGlnValIleLeuAs
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|1202 TATAATAAAATTATTAATCTAATGAGGAAA 1231
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LOCUS
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VERSION
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28 nArgAsnValAsnSerValHisMetProThrLys.....AlaValAspP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LPDHLIKDLFGDKEFLPQSAFLKWLGTHVCTHVILKELCGNLCFLLCGFNERNLNMSR
VDVYTTHSPAGTSVONMLHWSQAVKFQKFQAFDWGSSAKNYFHYNQSYPPTYNVKDML
VPTAVWSGGHDWLADVYDVNILLTQITNLVFHESIPEWEHLDFIWGLDAPWRLYNKII
                                                                                                                                                                                                                    Direct Submission
Submitted (05-APR-1994) Hong Du, Division of Human Genetics,
Children's Hospital Medical Center, 3333 Bernet Street, Cincinnati,
OH, 45229-3039, USA
                                                                                                                                   Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLGFILADAGFDVWMGNSRGNTWSRKHKTLSVSQDEFWAFSYDEMAKYDLPASINFIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NKTGQEQVYYVGHSQGTTIGFIAFSQIPELAKRIKMFFALGPVASVAFCTSPMAKLGR
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                                                                                                                                                                                                                                                                                                                                                                                                                     /cell_type="hepatoma"
/clone_lib="human liver HepG2 cDNA library/lambda ZAP"
14. 96
                                                                                          1 (bases 1 to 2481)
Du, H. and Gragory, G. M.
Structural Conservation of Putative Functional Motifs between and Human Lysosomal Acid Lipase
                                                         Craniata; Vertebrata; Eutele
Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acid lipase'
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LAL; lipase; lysosomal acid lipase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'product="lysosomal acid
'protein_id="CAA83495.1"
                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                        'db_xref="taxon:9606"
                                                      Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                          /clone="clone hLAL"
/tissue_type="liver"
                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                       /strain="HepG2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="LAL"
/citation=[1]
/replace="g"
2459. .2464
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/replace="c"
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Ratio: 3.875
Percent Similarity: 83.750
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US-09-333-159-47 x HSLYACLY
                                      Homo sapiens
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polyA_site
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                                    ORGANISM
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JOURNAL
KEYWORDS
SOURCE
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78

12 SerHisArgMetGluMetTrpLeuLeulleLeuValAlaTyrMetPheGl

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243
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                                                                                                                             175 AGTGAGGAATACCTAGTTGAGACAGAAGATGATATATTCTGTGCCTTAA 224
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                                                                                                                                                                                                            225 CCGAATTCCTCATGGGAGGAAGAACCATTCTGACAAAGGTCCCAAACCAG 274
                                                                                                                                                                                                                                             93 alValLeuLeuGlnHisGlyLeuValGlyGlyAlaSerAsnTrpIleSer 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                  hrLeuSerIleAspGlnAspGluPheTrpAlaPheSerTyrAspGluMet 159
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                                           roGluAlaPheMetAsnIleSerGluIleIleGlnH1sGlnGlyTyrPro
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                                                                                                                                                                                                                                                                                                                                  CGTGTGGATGGGCAACAGCAGGAAATACCTGGTCTCGGAAACATAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   475 GCAAAATATGACCTACCAGCTTCCATTAACTTCTTGAATAAAACTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   226 rLysPheLeuLeuLeuProAspMetMetIleLysGlyLeuPheGlyLysL
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                                                                                                                                                                            76 nArglleProArgGlyLeuValGlnProLysLysThrGlySerArgProV
                                                                                                                                                                                                                                                                                                               110 AsnLeuProAsnAsnSerLeuGlyPheIleLeuAlaAspAlaGlyPheAs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          875 CAACACATTCTCCTGCTGGAACTTCTGTGCAAAACATGTTACACTGGAGC
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692
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polyA_site
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                                                                                                   BASE COUNT
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                                                                                                                       ORIGIN
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Du, H. and Gregory, G.A.

Structural Conservation of Putative Functional Motifs between Mouse and Human Lysosomal Acid Lipase
Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         translation = "MKMRFLGLVVCLVLWTLHSEGSRGKLTAVDPETNMNVSEIISYW
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LPDHLIKDLFGDKEFLPQSAFLKWLGTHVCTHVILKELCGNLCFLLCGFNERNLNMSR
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VPTAVWSGGHDWLADVYDVNILLTQITNLVFHESIPEWEHLDFIWGLDAPWRLYNKII
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                      GTTCCATGAGAGCATTCCGGAATGGGAGCATCTTGACTTCATTTGGGCC 1174
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/clone=llne=HepG2 cDNA library/Lambda 2AP"
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/cell_type='hepatoma"
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                                                                                                                   rgAspMetThrValProThrAlaMetTrpThrGlyGlyGlnAspTrpLeu 359
                                                                                                                                                                                              SerAsnProGluAspValLysMetLeuLeuSerGluValThrAsnLeuIl 376
                                                                                                                                                                                                                                                                            eTyrHisLysAsnIleProGluTrpAlaHisValAspPheIleTrpGlyL 393
                                                                                                                                                                                                                                                                                                                                                         euAspAlaProHisArgMetTyrAsnGluIleIleHisLeuMetGlnGln 409
925 CAGGCTGTTAAATTCCAAAAGTTTCAAGCCTTTGACTGGGGAAGCAGTGC 974
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product="lysosomal acid lipase"
'protein_id="AAB60328.1"
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/product="lysosomal acid lipase"
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LOCUS HSU08464
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REFERENCE
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2459. .2464
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US-09-333-159-47 x HSU08464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nakagawa, H., Matsubara, S., Kuriyama, M., Yoshidome, H., Fujiyama, J., Yoshida, H. and Osame, M.
Cloning of rat lysosomal acid lipase cDNA and identification of the mutation in the rat model of Wolman's disease
J. Lipid Res. 36 (10), 2212-2218 (1995)
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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entry [NOB glbbsq 176569] from the original journal article.
This sequence comes from Fig. 2.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                         343 rgAspMetThrValProThrAlaMetTrpThrGlyGlyGlnAspTrpLeu
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                                                                                              CysGlyGlnValIleLeuAspGlnIleCysSerAsnIleMetLeuLeuLe
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                                                                                                                                                                uGlyGlyPheAsnThrAsnAsnMetAsnMetSerArgAlaSerValTyrA
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1. .3144
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Rattus sp.
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S81497
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US-09-333-159-47 x S81497
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109 SerAsnLeuProAsnAsnSerLeuGlyPheIleLeuAlaAspAlaGlyPh 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MMLYACLY 2358 bp mRNA. ROD 24-FEB-1999
M.musculus (C57 Black/6X CBA) LAL mRNA for lysosomal acid lipase.
231689
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1 (bases 1 to 2358)
Du.H., Witte,D.P. and Grabowski,G.A.
Tissue and cellular specific expression of murine lysosomal acid
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                                                                                          aGlyThrSerValGlnAsnIleLeuHisTrpSerGlnAlaValAsnSerG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                332 CysAsnGlnProThrProValArgTyrArgValArgAspMetThrValPr
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                                                                         ProAspMetMetIleLysGlyLeuPheGlyLysLysGluPheLeuTyrGl
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J. Lipid Res. 37 (5), 937-949 (1996)
96363957
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GFLLADRGFDVWMGNSRGNTWSLKHKTLSVSQDEFWAFSFDEWAKYDLPASINVILNK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 CATTGGGATCCTGCTTTCTCGGGTGCCCACGGGAACTGTATCAGCTGTGG 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 spProGluAlaPheMetAsnIleSerGluIleIleGlnHisGlnGlyTyr 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 ProCysGluGluTyrGluValAlaThrGluAspGlyTyrIleLeuSerVa 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75 lAsnArgileProArgGlyLeuValGlnProLysLysThrGlySerArgP 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 SerHisArgMetGluMetTrpLeuLeuIleLeuValAlaTyrMetPheGl 28
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Percent Identity: 54 217
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                                                                                                                                                                                                                                                                                               /product-"lysosomal acid lipase"
/protein_id-"CAA83494.1"
/db_xref-"GI:4456671"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lipase"
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                                                      /strain="C57 Black/6x CBA"
/db_xref="taxon:10090"
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Location/Qualifiers
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                                                                                               /sex="Female
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2358
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/gene="LAL"
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/gene="LAL"
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GTTTGGATGCCCCTGGAAACTGTATGATGAATAATCAGTCTAATGAAG 1200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alargaspMetThrValProThrAlaMetTrpThrGlyGlyGlnAspTrp 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LeuSerAsnProGluAspValLysMetLeuLeuSerGluValThrAsnLe 375
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ACAAACATTGACAACAGCAGCTTGGGCTTCCTCCTGGCGGATCGTGGCTT 350
                                                                                          351 TGATGTGTGGATGGGAAACAGCAGAGGAAACACCTGGTCTCTGAAGCACA 400
                                                                                                                                                                                                         MetalaargPheaspLeuProalaValIleasnPheIleLeuGlnLysTh 175
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                                                       eAspValTrpMetGlyAsnSerArgGlyAsnAlaTrpSerArgLySHisL 142
                                                                                                                                ysThrLeuSerIleAspGlnAspGluPheTrpAlaPheSerTyrAspGlu 158
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05-APR-1995
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Benicourt,C., Blanchard,C. and Junien,J.L.
Recombinant gastric lipase from rabbit and pharmaceutical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93 alValLeuLeuGlnHisGlyLeuValGlyGlyAlaSerAsnTrpIleSer 109
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Precursor of rabit gastric lipase coding sequence.
A26689
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 AAATACCAGTGAATGCTGGACTTGAATACTTCCCTTCAGAGGGGG 1245
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287 c 276 g
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/organism-"synthetic
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Ratio: 3.505
Percent Similarity: 82.836
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US-09-333-159-47 x A26689
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                                 seq_name: gb_pat:1:A26689
                                                                       seg_documentation_block:
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ACCESSION
VERSION
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SOURCE
ORGANISM
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ORIGIN
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1201
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489 176 539 589 210

193

226 689 243 260

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Location/Qualifiers
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   synthetic construct
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US-09-333-159-47 x A26690/rev
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Milarity: 82.836
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176
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                                                                                                                               209
                                                                                                                                                                                                                                                          rLysPheLeuLeuLeuProAspMetMetIleLysGlyLeuPheGlyLysL 243
                                                                                                                                                                                                                                                                                                                         ysGluPheLeuTyrGlnThrArgPheLeuArgGlnLeuValIleTyrLeu 259
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AlaArgPheAspLeuProAlaValIleAsnPheIleLeuGlnLysThrGl
                              GCTAAATATGACCTTCCAGCCACAATTGACTTCATTGTAAAGGAAACTGG
                                                                                                                           hellealaPheSerThrMetProGluLeuAlaGlnLysIleLysMetTyr
                                                                                             ACAGGAAAAGCTGCACTATGTTGGTCATTCCCAGGGCACCACCATTGGTT
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Precursor of rabit gastric lipase (comp.).
A26690.1 GI:905030
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LOCUS A26690
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DEFINITION ACCESSION VERSION KEYWORDS SOURCE

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artificial sequence.
I (bases 1 to 1378)
Benicourt,C., Blanchard,C. and Junien,J.L.
Recombinant gastric lipase from rabbit and pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1091
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AlaArqPheAspLeuProAlaValIleAsnPheIleLeuGlnLysThrGl 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hellealaPheSerThrMetProGluLeuAlaGlnLysIleLysMetTyr 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1281 AACTACACATGGTCTTTTGGAAAATCAGCACCAACA......AACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32 nSerValHis......metProThrLysAlaValAspP
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Percent Identity: 54.478
                                                                                                                                                                                                                                                                                                                                                                                                                                                               construct"
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                                                                                                                                                                                                        compositions
Patent: EP 0542629-A 10 19-MAY-1993;
INSTITUT DE RECHERCHE JOUVEINAL
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                                                                                                                                                                                                             YLGHNPAGTSVQDFLHWAQLVRSGKFQAFNWGSPSQNMLHYNQKTPPEYDVSAMTVPV
AVWNGGNDILADPQDVAMLLPKLSNLLFHKEILAYNHLDFIWAMDAPQEVYNEMISMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54 ACATGGCCTATTTGGAAAACTGGGTCCTGGAAAACCCTGAAGCAAATATGA 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nSerAryGlyAsnAlaTrpSerArgLysHisLysThrLeuSerIleAspG 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rTyrValGlyTyrSerGlnGlyThrThrMetGlyPhe1leAlaPheSerT 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        isGlyLeuValGlyGlyAlaSerAsnTrpIleSerAsnLeuProAsnAsn 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 AAGATGTGCCTGTTATTAATAACAAGTGTGATATCAACATTCGGAGGTGC
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'db_xref="taxon:10116"
'. .1194
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                                  /codon_start=]
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Ratio: 3.556
nilarity: 82.206
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US-09-333-159-47 x A01157
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ORIGIN
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                  CDS
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Sciurognathi; Muridae; Murinae;
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protein.
                                                                                                 CAGGCTGTTAAATCTGGAAATTTTCAAGCTTTTAATTGGGGAAGTCCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  390 TCAGAATGTAGTGCACTTCAATCAGCCCACACCTCCCTACTACTACTAGTGA
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                                                                                                                                                   ysGluPheLeuTyrGlnThrArgPheLeuArgGlnLeuValIleTyrLeu
                                                                                                                                                                                      640 AAATATTCTACCCACACAATTTCTTTGATCAATTTCTTGCCACTCAAGTG
                                                                                                                                                                                                                        260 CysGlyGlnValIleLeuAspGlnIleCysSerAsnIleMetLeuLeuLe
                                                                                                                                                                                                                                                                                              276 uGlyGlyPheAsnThrAsnAsnMetAsnMetSerArgAlaSerValTyrA
                                                                                                                                                                                                                                                                                                                                                                    293 laAlaHisThrLeuAlaGlyThrSerValGlnAsnIleLeuHisTrpSer
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/organism="Rattus norvegicus"
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Williamson, R.
Patent: WO 8500381-A 3 31-JAN-1985;
CellTech Ltd
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Nattus norvegicus
Rattus norvegicus
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA
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LOCUS A01157
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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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81

64

453

181

403 164

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49. .1236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATGGTTTGATCGCATCAGCCACAAACTGGATTGCAAATCTACCAAACAAC 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   131 nSerArgGlyÄsnAlaTrpSerArgLysHisLysThrLeuSerIleAspG 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98 isGlyLeuValGlyGlyAlaSerAsnTrpIleSerAsnLeuProAsnAsn 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       148 InAspGluPheTrpAlaPheSerTyrAspGluMetAlaArgPheAspLeu 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAAGAATAATTCTGAAAATATAGGCAAGAGACCTGTGGTGTATTTGCAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46 AAGATGTGCTGTTATTAATAACAAGTGTGATATCAACATTCGGAGGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96 ACATGGCCTATTTGGAAAACTGGGTCCTGGAAACCCTGAAGCAAATATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   snileSerGluileIleGlnHisGlnGlyTyrProCysGluGluTyrGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81 yLeuValGlnProLysLysThrGlySerArgProValValLeuLeuGlnH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 GluMetTrpLeuLeuIleLeuValAlaTyrMetPheGln...ArgAsnVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31 lAsnSerValHisMetProThrLysAlaValAspProGluAlaPheMetA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="aa 153 pot. lipid binding site"
1355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps: 1
Percent Identity: 54.637
                                 /organism="Rattus norvegicus"
/db_rref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                             /product="lipase (aa 1-377)"
505. .507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           387
                                                                                                                                                                                           /protein_id="CAA26179.1"
/db_xref="GI:56596"
                                                                                                                                                    /note="lipase precursor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to: 1355
Cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="polyA site"
291 c 276 g
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                                                                                                                                                                          /codon_start=
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82.206
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US-09-333-159-47 x RNLIP
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Percent Similarity:
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                                                                                      sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores
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                          source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             396
    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGIN
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Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 1355)
Docherty, A.J., Bodmer, M.W., Angal, S., Verger, R., Riviere, C.,
Lowe, P.A., Lyons, A., Emtage, J.S. and Harris, T.J.
Molecular cloning and nucleotide sequence of rat lingual lipase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAR-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1104 TCTTGCCTACAATCACCTGGACTTCATCTGGGCAATGGATGCCCCTCAAG 1153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         954 CTACAACCAGAAAAGGCCTCCTGAATATGATGTGTCAGCCATGACTGTGC 1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         331 sCysAsnGlnProThrProValArgTyrArgValArgAspMetThrValP 348
                                                                                                                                                                                                                                                                                      ValLysMetLeuLeuSerGluValThrAsnLeuIleTyrHisLysAsnIl 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 eProGluTrpAlaHisValAspPheIleTrpGlyLeuAspAlaProHisA 398
    214
                                                                                        231
                                                                                                                                                                                                  LeuAspGlnIleCysSerAsnIleMetLeuLeuLeuGlyGlyPheAsnTh 281
                                                                                                                                                                                                                                                                                                                                                                                     CTAGATCTTCTCTCCAGCAACACTTTATTCATCTTCTGTGGATTTGACAA 803
                                                                                                                                                                                                                                                                                                                                                                                                                                 281 rAsnAsnMetAsnMetSerArgAlaSerValTyrAlaAlaHisThrLeuA 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      laGlyThrSerValGlnAsnIleLeuHisTrpSerGlnAlaValAsnSer 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GlyGluLeuArgAlaPheAspTrpGlySerGluThrLysAsnLeuGluLy 331
                                          554 CCAATCCTACACTGGCCAAAAAATCAAGACGTTTTATGCATTAGCTCCA 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       398 rgMetTyrAsnGluIleIleHisLeuMetGlnGlnGluGluThrAsn 413
    hrMetProGluLeuAlaGlnLysIleLysMetTyrPheAlaLeuAlaPro
                                                                                        215 IleAlaThrValLysHisAlaLysSerProGlyThrLysPheLeuLeuLe
                                                                                                                                604 GITGCIACCGIGAAGIATACACAAAGICCCTIGAAAAAAAATITCATITAI
                                                                                                                                                                        uProAspMetMetIleLysGlyLeuPheGlyLysLysGluPheLeuTyrG
                                                                                                                                                                                                                                                            lnThrArgPheLeuArgGlnLeuValIleTyrLeuCysGlyGlnValIle
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85215587
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Rat mRNA for lingual lipase.
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ACCESSION
VERSION
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AUTHORS
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COMMENT
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SOURCE
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                                                                                                                                                                                                                                                            248
                                                                                                                                                                                                                                                                                                                                                                                       754
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and

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AFILADAGYDVWLGNSRGNIWARRNLYYSPOSVEFWRESFDEMAKYDLPATIDFILKK
TGODKLHYVGHSQGTTIGFTAFSTHRKLARRIKTRYALAPVATVKYTETLLAKLMLVP
STEKLIFGNK IFYPHFFDOFLATEVCSRETVOLLCSNALPITGFFDNLMARRLD
VYLGHNPAGTSVQNYLWSGAKYGKFGAFDWGSPYQNMHHYQSMPPYYNLTDMHVP
IAVWNGGNDLLADPHDVDLLLSKLPNLIYHRKIPPYNHLDFIWAMDAPQAVYNEIVSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAEEY EVVTEDGY ILGIDRI PYGRKNSENIGRRPVAFLOHGLLASATNWI SNLPNNSL
                                                                                                                                                                                                                       Submitted (10-JUN-1997) C. Benicourt, Ecole Normale Superieure de Cachan, L.I.R.B.A (Laboratoire Interdisciplinaire de Recherche en Biologie Appliquee), 61 avenue du President Wilson, F-94235 Cachan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation-"MWLLLTAASVISTLGTTHGLFGKLHPTNPEVTMNISQMITYWGY
  . Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Eutheria, Carnivora, Fissipedia, Canidae, Canis.
                       1 (bases 1 to 1651)
Vaganay, S., Joliff, G., Bertaux, O., Toselli, E., Devignes, M.D. Benicourt, C.
                                                                                                 The complete cDNA sequence encoding dog gastric lipase DNA Seq. 8 (4), 257-262 (1998) 99450174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101 CACACATGGTTTATTTGGAAAATTACATCCCACA......AACCCTG 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44 luAlaPheMetAsnIleSerGluIleIleGlnH1sGlnGlyTyrProCys 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17 MetTrpLeuLeuIleLeuValAlaTyrMetPheGlnArgAsnValAsnSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..MetProThrLysAlaValAspProG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  product="triacylglycerol lipase"
protein_id="CAA74198.1"
                                                                                                                                                                                                                                                                                                                                        /organism="Canis familiaris"
/db_xref="taxon:9615"
/dev_stage="adult"
/tissue_type="stomach mucosa"
54. 1250
/gene="DGL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="SWISS-PROT:P80035"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /evidence-experimental
111. 1247
/gene-"DGL"
1602. 1607
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          number-"3.1.1.3"
                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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419 c
                                                                                                                                                              2 (bases 1 to 1651)
Benicourt, C.
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/gene="DGL"
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                                                                                                                                                                                                          Direct Submission
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Ratio: 3.486
Percent Similarity: 83.166
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US-09-333-159-47 x CFLIPASE
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                                                                                               TITLE
JOURNAL
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1146 TCTTGCCTACAATCACCTGGACTTCATCTGGGCAATGGATGCCCCTCAAG 1195
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                                                                                                                                                              198 hrMetProGluLeuAlaGlnLysIleLysMetTyrPheAlaLeuAlaPro 214
                                                                                                                                                                                                                                                   215 IlealaThrvalLysHisalaLysSerProGlyThrLysPheLeuLeuLe 231
                                                                                                                                                                                                                                                                                                                                 uProAspMetMetIleLysGlyLeuPheGlyLysLysGluPheLeuTyrG 248
                                                                                                                                                                                                                                                                                                                                                                                                                    InThrArgPheLeuArgGlnLeuValIleTyrLeuCysGlyGlnValIle 264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   846 GAAAAACTTAAATGTGAGTGTTTGATGTGTATCTAGGGCATAATCCAG 895
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DGL gene; gastric lipase; triacylglycerol lipase.
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281 rAsnAsnMetAsnMetSerArgAlaSerValTyrAlaAlaHisThrLeuA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         298 laGlyThrSerValGlnAsnIleLeuHisTrpSerGlnAlaValAsnSer
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                                                                                                                                      181 rTyrValGlyTyrSerGlnGlyThrThrMetGlyPheIleAlaPheSerT
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Canis familiaris mRNA for lipase.
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LOCUS DEFINITION ACCESSION VERSION KEYWORDS

SOURCE

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Gaps: Identity: Length:

to: 1651

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0 0 0 0 0	ITTPMetGlyAsnSerargGlyAsnAlaTrpSerargLysHisLysThrL	nGluLySIleTyTTyrValGlyTyrSerGlnGlyThrThrMetGlyPheI 19 ::: ::::	SPheLeuLeuLeuProAspMetMetIleLysGlyLeuPheGlyLysLysG 24. :::: :: :: :: ACTCATGCTCGTTCGTTCTTCAAGCTTATATTTGGAAACAAA 74. uPheLeuTyrGlnThrArgPheLeuArgGlnLeuVallleTyrLeu 25:	udlyGlyPheAsnThrAsnAsnMetAsnMetSerArgAlaSerValTyrA 2:	TLYSASNLEUGIULYSCYSASNGINPrOThrProValargTyrargVala 3: :::
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Unknown,
Unclassified.
1 (bases 1 to 1137)
Blanchard,C., Benicourt,C. and Junien,J.
Blanchard,C., Benicourt,C. and Junien,J.
Nucleic acids encoding dog gastric lipase and their use for the production of polypeptides
Patent: US 507726-A 2 15-SEP-1998;
Location/Qualifiers
1. 1137
                                                                                                                                                                    29-SEP-1999
103 yAlaSerAsnTrpIleSerAsnLeuProAsnAsnSerLeuGlyPheIleL 120
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                                                          Length: 372
Gaps: 3
Percent Identity: 56.452
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Sequence 2 from patent US 5807726.
AR039022 GI:5958385
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Ratio: 3.624
Percent Similarity: 84.677
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VERSION
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Blanchard,C., Benicourt,C. and Junien,J.
Polypeptide derivatives of dog gastric lipase and pharmaceutical compositions containing same patent: US 5998189-A 2 07-DEC-1999;
Location/Qualifiers
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US-09-333-159-47 x AR092633
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FEATURES
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LOCUS AR092633 1137 bp DNA
DEFINITION Sequence 2 from patent US 5998189.
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153

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to: 1137

372 3

Length: Gaps:

284

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helleLeuGlnLysThrGlyGlnGluLysIleTyrTyrValGlyTyrSer 186
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1 (bases 1 to 1140)
Blanchard,C., Benicourt,C. and Junien,J.
Nucleic acids encoding dog gastric lipase and their use for the production of polypetides
Patent: US 5807726-A 4 15-SEP-1998;
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                       657 TCAATTTCTCGCCACGAGGTATGCTCCCGCGAGACGGTGGATCTCCTCT
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Gaps: 3
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Sequence 4 from patent US 5807726.
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1110 AATTGTTTCCATGATG 1125
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                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 1140)
Blanchard, C., Benicourt, C. and Junien, J.
Polypeptide derivatives of dog gastric lipase and pharmaceutical compositions containing same
Patent: US 5998189-A 4 07-DEC-1999;
                                                                                                                                                                                                                                                                                                                          08-SEP-2000
910 ATGCCTCCTACTACAACCTGACAGACATGCATGTGCAATGGCAGTGTG 959
                                                                                                   euSerGluValThrAsnLeuIleTyrHisLysAsnIleProGluTrpAla 385
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                                         PThrGlyGlyGlnAspTrpLeuSerAsnProGluAspValLysMetLeuL
                                                          1010 TITCCAAGCTCCCCAATCTCATTTACCACAGGAAGATTCCTCCTTACAAT
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Sequence 4 from patent US 5998189.
AR092634
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308 c 250 g
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Ratio: 3.624
illarity: 84.677
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US-09-333-159-47 x AR092634
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LOCUS AR092634
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                                                                          aPheSerTyrAspGluMetAlaArgPheAspLeuProAlaValIleAsnP
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                                              TrpSerArgLysHisLysThrLeuSerIleAspGlnAspGluPheTrpAl
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                                                                                                                                                                                                                                                                                            GlnGly?hrThrMetGlyPheIleAlaPheSerThrMetProGluLeuAl
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377 470 167 24(25;

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Gene therapy; TANGO protein; INTERCEPT protein; neurological disorder; central nervous system; focal brain disorder; bipolar affective disorder; plobal-diffuse cerebral disorder; cerebrovascular; Alzheiner's disease; senile dementia; Huntington's disease; amyotrophic lateral sclerosis; Parkinson's; Gilles de la Tourette's syndrome; hypertension; sleep; neuropsychiatric; psychoactive substance use; anxiety; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to TANGO or INTERCEPT proteins and coding sequences (see AAF45121-F45136 and AAF45138-F45139 and AAB66031-B66057, AAB66004-E66083 and AAB66085). The TANGO/INTERCEPT proteins and coding sequences are useful for the treatment of neurological disorders such as central nervous system (CNS) disorders, CNS-related disorders, focal brain disorders, global-diffuse cerebral disorders and other neurological and cerebrovascular disorders. The CNS disorders include Alzheimer's disease, senile dementia, Huntington's disease, amyotrophic
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1.66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TANGO and INTERCEPT nucleic acids, proteins, and antibodies, useful for screening assays and diagnostic assays and for the treatment of neurological diseases such as Alzheimer's, Parkinson's and Huntington's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lateral sclerosis, Parkinson's, Gilles de la Tourette's syndrome, autonomic function disorders such as hypertension and sleep disorders,
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 153.51
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/SIDS8/gcgdata/jeneseq/geneseqn/NA1999.DAT:AAX81263
/SIDS8/gcgdata/jeneseq/geneseqn/NA2000.DAT:AAC69112
/SIDS8/gcgdata/jeneseq/geneseqn/NA1998.DAT:AAV35458
/SIDS8/gcgdata/jeneseq/geneseqn/NA1998.DAT:AAX35473
/SIDS8/gcgdata/jeneseq/geneseqn/NA1999.DAT:AAX08414
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AAF45132 standard; cDNA; 1269
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US-09-333-159~47 x AAF45132
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P-PSDB; AAB66065.
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of: US-09-333-159-47 to: N_Geneseq_0601:*
                                                              Results were produced by the GenCore Copyright (c) 1993-2000 Compugen Ltd.
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Database: N.Geneseq_0601:*
Database sequences: 730101
Database length: 313950809
Search time (sec): 113.380000
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                                              GAAATCATCCAACATCAAGGCTATCCCTGTGAGGAATATGAAGTCGCAAC 200
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                                                                                                                                                                                                                                                                                      lileAsnPheileLeuGlnLysThrGlyGlnGluLysIleTyrTyrValG 184
                                                                                                                                                                                                                                                                                                                                                                                                        217 rValLysHisAlaLysSerProGlyThrLysPheLeuLeuLeuProAspM 234
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          GluileileGlnHisGlnGlyTyrProCysGluGluTyrGluValAlaTh
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MetLeuGluThrLeuSerArgGlnTrpIleValSerHisArgMetGluMe
                                     tTrpLeuLeuIleLeuValAlaTyrMetPheGlnArgAsnValAsnSerV
                                                                           alHisMetProThrLysAlaValAspProGluAlaPheMetAsnIleSer
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Gene therapy; TANGO protein; INTERCEPT protein; neurological disorder; central nervous system; focal brain disorder; bipolar affective disorder; global-diffuse cerebral disorder; cerebrovascular; Alzhelmer's disease; senile dementia; Huntington's disease; amyotrophic lateral sclerosis; Parkinson's; Gilles de la Tourette's syndrome; hypertension; sleep; neuropsychiatric; psychoactive substance use; anxiety; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TANGO and INTERCEPT nucleic acids, proteins, and antibodies, useful for screening assays and diagnostic assays and for the treatment of neurological diseases such as Alzheimer's, Parkinson's and Huntington's
                                                                                                                                                                                     1100
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                                                                                                                                                                                                                                                                   rpalaHisValAspPheIleTrpGlyLeuAspAlaProHisArgMetTyr 400
                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: /SIDS8/gcgdata/geneseq/geneseqn/nA2001.DAT:AAF45131
                                                                 GCTGCTCTCTGAGGTGACCACCTCATCTACCATAAGAATATTCCTGAAT
                                                  tLeuLeuSerGluValThrAsnLeuIleTyrH1sLysAsnIleProGluT
                                                                                                                                                                                                                                                                                  MetTrp1hrGlyGlyGlnAspTrpLeuSerAsnProGluAspValLysMe
ServalGlnAsnIleLeuHisTrpSerGlnAlavalAsnSerGlyGluLe
                         TCTGTGCAAAATATTCTACACTGGAGCCAGGCAGTGAATTCTGGTGAACT
                                                                                                       InProThrProValArgTyrArgValArgAspMetThrValProThrAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
ID AAF45131 standard; cDNA; 2044
                                                                                                                                                                                                                                                                                                                                                                                                   1251 ACGGTGTGAGGCCGTATTG 1269
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The present invention relates to TANGO or INTERCEPT proteins and coding sequences (see AAF45121-F44136 and AAF45139-F45139 and AAB66031-B66057, AAB66048-B66083 and AAB66085). The TANGO/INTERCEPT proteins and coding sequences are useful for the treatment of neurological disorders such as central nervous system (CNS) disorders, CNS-related disorders, focal neurological and cerebrovascular disorders and other neurological and cerebrovascular disorders and other lateral and cerebrovascular disorders. The CNS disorders include Alzheimer's disease, senile dementia, Huntington's disease, amyotrophic autonomic function disorders such as hypertension and sleep disorders, neuropsychiatric disorders such as hypertension and sleep disorders, anxiety, and bipolar affective disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        126 ATGTTGGAAACCTTGTCAAGACAGTGGATTGTCTCACACAGAATGGAAAT 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     226 TACATATGCCAACTAAAGCTGTGGACCCAGAAGCATTCATGAATATTAGT
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                                                                                                                                                                                                                Sequence 2044 BP; 618 A; 401 C; 460 G; 565 T; 0 other
                                                                                                                                                                                                                                                                              Length: 423
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                             to: 2044
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Ratio: 5.312
Percent Similarity: 100.000
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US-09-333-159-47 x AAF45131
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676 GCTATTCACAGGGCACCACCATGGGCTTTATTGCATTTTCCACCATGCCA 725
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hydrolysis; transesterification; ds.
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                              1276 GGGCTCACGTGGATTTCATCTGGGGTTTGGATGCTCCTCACGTATGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1326 AATGAAATCATCCTGATGCAGCAGGAGGAGACCAACCTTTCCCAGGG
                                                                                                     etMetIleLysGlyLeuPheGlyLysLysGluPheLeuTyrGlnThrArg
                                                                                                               PheteuargGlnLeuValIleTyrLeuCysGlyGlnValIleLeuAspGl
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                  GluLeuAlaGlnLysIleLysMetTyrPheAlaLeuAlaProIleAlaTh
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ID AAQ42310 standard;
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AsnLeuProAsnAsnSerLeuGlyPheIleLeuAlaAspAlaGlyPheAs
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                                                                                                                                                                                                                                                                                                                                                                                                                        193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA was isolated from rabbit gastric mucosal cells, converted to CDNA and fragments cloned in pUC18. Recombinant plasmids were used to transform E.coll MA294 and cells screened for reactivity with probes corresp. to known parts of the RGL sequence. One positive clone contd. plasmid pJ0101 which contd. a 1.35 kb pstI sequence. This fragment was isolated, subjected to PCR and the amplification prod. ligated with the 2.2 kb BgIII-SacI fragment of pR0276 (contg. a synthetic Tac promoter and transcription stop signal). The recombinant plasmid was designated PRGLN2.1.
                                                                                                                                                                                                                                                                                                                                                                                                                  Rabbit gastric lipase, its precursor and their DNA - useful for treating conditions linked to gastric lipase deficiency, such as mucoviscidiosis and pancreatic exocrine insufficiency
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Percent Identity: 54.478
                                                        /note- "claim 1; page 10-11"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                        RECH JOUVEINAL
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82.836
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Ratio: 3.505
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US-09-333-159-47 x AAQ42310
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P-PSDB; AAR37302.
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                        misc_RNA
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989 TCAGAATGTAGTGCACTTCAATCAGCCCACACCTCCCTACTACAATGTGA 1038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              739 AAATATICTACCCACACAATTICTTIGATCAATTICTIGCCACTCAAGIG 788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     839 TTGTGGCTTTGACAGCGCAAACTTGAACATGAGTCGCTTGGATGTGTACG 888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    889 TGTCACATAATCCGGCAGGAACTTCAGTTCAAAACATGCTGCACTGGACC 938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       326 rLysAsnLeuGluLysCysAsnGlnProThrProValArgTyrArgValA 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   360 SerAsn?roGluAspValLysMetLeuLeuSerGluValThrAsnLeuIl 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    eTyrHisLysAsnIleProGluTrpAlaHisValAspPheIleTrpGlyL 393
                                                                                                                                                                                                                                                                           160 AlaArgPheAspLeuProAlaValIleAsnPheIleLeuGlnLysThrGl 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       293 laAlaHisThrLeuAlaGlyThrSerValGlnAsnIleLeuHisTrpSer 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       euaspalaProHisArgMetTyrasnGluIleIleHisLeuMetGlnGln
                                                                                                                                                                                                                                                                                                     489 GCTAAAIATGACCTTCCAGCCACAATTGACTTCATTGTAAAGGAAACTGG
                                                                                                                                                                                                                                                                                                                                                                                                        276 uGlyGlyPheAsnThrAsnAsnMetAsnMetSerArgAlaSerValTyrA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             310 GlnAlaValAsnSerGlyGluLeuArgAlaPheAspTrpGlySerGluTh
                                                                      126 pvaltrpmetGlyasnSerargGlyasnAlaTrpSerargLysH1sLysT
                                                                                                                     389 TGTGTGGCTGGGGAACAGCAGAGGAAATACCTGGTCCAGAAGAAACTTAT
                                                                                                                                                                          143 hrLeuSerIleAspGlnAspGluPheTrpAlaPheSerTyrAspGluMet
                                                                                                                                                                                                                                                                                                                                                                            176 yGlnGluLysIleTyrTyrValGlyTyrSerGlnGlyThrThrMetGlyP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               helleAlaPheSerThrMetProGluLeuAlaGlnLysIleLysMetTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             226 rLysPhaLeuLeuProAspMetMetIleLysGlyLeuPheGlyLysL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ysGluPheLeuTyrGlnThrArgPheLeuArgGlnLeuValIleTyrLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     260 CysGly3lnValIleLeuAspGlnIleCysSerAsnIleMetLeuLeuLe
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86

81

81

204 GAAGAATAATTCTGAAATATAGGCAAGAGACCTGTGGTGTATTTGCAGC

303

isGlyLeuValGlyGlyAlaSerAsnTrpIleSerAsnLeuProAsnAsn 114

nSerAryGlyAsnAlaTrpSerArgLysHisLysThrLeuSerIleAspG

131

453

ProAlaValIleAsnPheIleLeuGlnLysThrGlyGlnGluLysIleTy 181

165

104

148 InAspGluPheTrpAlaPheSerTyrAspGluMetAlaArgPheAspLeu

164

410 GluGlu 411

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This sequence may be expressed in a transformant host organism using a vector plasmid in order to produce a prelingual lipase protein. The expressed protein may be used for the treatment of lipase deficiency.
                                                                                                                                                                                                                                                                                                                                                   New lingual lipase protein for treatment of lipase deficiency - also new pre-lingual lipase protein and related products
                   seq_name: /SIDS8/gcgdata/geneseq/geneseqn/nA1985.DAT:AAN50385
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1336 BP; 409 A; 285 C; 263 G; 379 T; 0 other;
                                                                                                                           88
                                                                                                                        Prelingual lipase; enzyme; EC-3.1.1.3;
                                                                                                                                                              Location/Qualifiers 7..1194
                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 5; 15pp; English.
                                  BP
1239 GATAAA 1244
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503
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                                                                                                                                                                                                            LeuAspGlnIleCysSerAsnIleMetLeuLeuGlyGlyPheAsnTh 281
                                                                                                                                                                                                                                                                                    314
                                                                                                                                                                                                                                                                                                                         331
                                                                                                                                   231 uProAspMetMetIleLysGlyLeuPheGlyLysLysGluPheLeuTyrG :||| ::::::::||| | |||||| |||||| : 654 TCCTACATTCTTTCAAGCTTATGTTTGGCAAGAAAATGTTCTGCCC
                                                                                                                                                                                                                                              GlyGluLeuArgAlaPheAspTrpGlySerGluThrLysAsnLeuGluLy
|||::::::::|||||||:::||||||||
hrMetProGluLeuAlaGlnLysIleLysMetTyrPheAlaLeuAlaPro
                                                                         IlealaThrValLysHisAlaLysSerProGlyThrLysPheLeuLe
                                                                                                                                                                        248 InThrArgPheLeuArgGlnLeuValIleTyrLeuCysGlyGlnValIle
                                                                                                                                                                                                                                                                                                                                                            sCysAsnGlnProThrProValArgTyrArgValArgAspMetThrValP
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       454
                                                             198
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31 lAsnSerValH1sMetProThrLysAlaValAspProGluAlaPheMetA 48

16 GluMetTrpLeuLeuIleLeuValAlaTyrMetPheGln...ArgAsnVa 31

from: 1 to: 1336

alignment_block: US-09-333-159-47 x AAN50385 Align seg 1/1 to: AAN50385

Length: 399
Gaps: 1
Percent Identity: 54.386

Ouality: 1158.50 Ratio: 3.543 Allarity: 81.955

Ratio: Percent Similarity:

alignment_scores:

+ AAGATGTGGCTGTTATTAATAACAAGTGTGATATCAACATTCGGAGGTGC

104 ATATTAGTCAGATGATAACTTACTGGGGATATCCATGTCAAGAATATGAA 153

snileSerGluilelleGlnHisGlnGlyTyrProCysGluGluTyrGlu 64

Percent Identity: 56.452

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84.677
                             alignment_block:
US-09-333-159-47 x AAQ68388
                                                                          Align seg 1/1 to: AAQ68388
 Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cGL is used to improve absorption of ingested fat, in healthy and sick patients (e.g. having altered levels of gastric lipase); to treat conditions associated with insufficiency (or lack) of lipases, esp. mucoviscidosis or exocrine pancreatic insufficiency and partic. Where immobilised, for bloconversions, e.g. hydrolysis or transesterification (other mammalian gastric lipases, or derivs, can be used in this application).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence given below is the sequence of figure 8, altered according to the amendments described on page 2 of the appended
                                                                                                                                                                                                                                                                                                                                              Canine gastric lipase; CGL; dog; fat; mucoviscidosis; enzyme; bloconversion; exocrine pancreatic insufficiency; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant canine gastric lipase and nucleic acid encoding are used for improving absorption of ingested fat, treating mucoviscidosis etc. and in enzymatic bio-conversions
                 381 eProGluTrpAlaHisValAspPheileTrpGlyLeuAspAlaProHisA 398
365 ValLysMetLeuLeuSerGluValThrAsnLeuIleTyrHisLysAsnIl 381
                                                                                                                                              1154 AGGTTTACAATGAGATGATTTCCATGATGGCAGAAGAACTAAAAGAAT 1200
                                                                                                                                                                           seq_name: /SIDS8/gcgdata/geneseq/geneseqn/NA1994.DAT:AAQ68388
                                                                                                                 rgMetTyrAsnGluIleIleHisLeuMetGlnGlnGluGluThrAsn 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1528 BP; 394 A; 386 C; 328 G; 420 T; 0 other
                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= b
/note= "claim 1,"
                                                                                                                                                                                                         seq_documentation_block:
ID AAQ68388 standard; DNA; 1528 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93WO-FR01260
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                                                                                                                                                                                                                                                                                    (first entry)
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/*tag=
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/*tag= 1
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P-PSDB; AAR56870.
                                                                                                                                                                                                                                                                                                                                                                                        Canis familiaris.
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                                                                                                                                                                                                                                                                                  20-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9413816-A
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                                                                                                                                                                                                                                                      AAQ68388;
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Length: Gaps:

Quality: 1141.50 Ratio: 3.624

alignment_scores:

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359
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                                                                                                          203 aGlnLyslleLysMetTyrPheAlaLeuAlaProIleAlaThrValLysH 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  706
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 302 IGInAsnIleLeuHisTrpSerGinAlaValAsnSerGlyGluLeuArgA 319
                                                                                                                                                                                                                                                                  103
                                                                                                                                                                                                                                                                                                                                                                                  259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            153 aPheSerTyrAspGluMetAlaArgPheAspLeuProAlaValIleAsnP 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              707 GCAGCAACGCCCTGTTTATCATTTGTGGATTTGACACTATGAACTTGAAC 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MetSerArgAlaSerValTyrAlaAlaHisThrLeuAlaGlyThrSerVa 302
                                                                                                                                                                                        86
                                                                                                                                                                                                                                                                                                                                            70 lyTyrIleLeuSerValAsnArgIleProArgGlyLeuValGlnProLys
                                                                                                                                                                                                                  110 GTTATATCCTTGGGATCGACAGAATTCCTTATGGGAGAAAATTCAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19 CCCACA......AACCCTGAAGTGACCATGAATATAAGTCAGATGAT
                                                                                                                                                                                                                                                                  87 LysThrGlySerArgProValValLeuLeuGlnHisGlyLeuValGlyGl
                                                                                                                                                                                                                                                                                        160 AATATAGGCCGGAGACCTGTTGCATTTTTGCAACACGGTTTGCTCGCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        170 helleLeuGlnLysThrGlyGlnGluLysIleTyrTyrValGlyTyrSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    187 GlnGlyThrThrMetGlyPheIleAlaPheSerThrMetProGluLeuAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          220 isAlaLysSerProGlyThrLysPheLeuLeuLeuProAspMetMetIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                560 ACACCGRAACCCTGTTAAACAAACTCATGCTCGTCCCTTCGTTCCTCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      237 LysGlyLeuPheGlyLysLysGluPheLeuTyrGlnThrArgPheLeuAr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        610 AAGCTTATATTTGGAAACAAAATATTC...TACCCACACCACTTCTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          269 ysSerAsnIleMetLeuLeuLeuGlyGlyPheAsnThrAsnAsnMetAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          757 ATGAGTCGCTTGGATGTGTATCTGTCACATAATCCAGCAGGAACATCGGT
                                    37 ProThrLysAlaValAspProGluAlaPheMetAsnIleSerGluIleIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    137 TrpSerArgLysHisLysThrLeuSerIleAspGlnAspGluPheTrpAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              253 gGln...LeuValIleTyrLeuCysGlyGlnValIleLeuAspGlnIleC
to: 1528
from: 1
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plants producing recombinant lipase in an enzymatically active form.

Alternatively the first 12 bases of this sequence (encoding amino acids 1-4 of the protein encoded by this sequence) or bases 1-162 of this sequence (encoding amino acids 1-54) can be deleted to form the derivatives designated delta-4 or delta-54 respectively. Plants, or their extracts, expressing the lipases or the truncated derivatives, can be used: (a) as pharmaceuticals or food to facilitate absorption of fat, either in healthy subjects or in patients with inadequate levels of astric/pancreatic insufficient, in the elderly or in patients undergoing medical treatment which alters fat adsorption; (b) for performing industrial or gricultural reactions, e.g. in processing of fats or in the dairy industry, for hydrolysis or transesterification reactions, etc., where the plant naterial may provide both enzyme and substrate. The transgenic plants can also be used for biofuel production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 210 AGCCACAAACTGGATCTCCAACCTGCCCAACAACAGCCTGGCCTTCATCC 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         153 aPheSerTyrAspGluMetAlaArgPheAspLeuProAlaValIleAsnP 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       helleLeuGlnLysThrGlyGlnGluLysIleTyrTyrValGlyTyrSer 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 yalaSerAsnTrpIleSerAsnLeuProAsnAsnSerLeuGlyPheIleL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       euAlaAspAlaGlyPheAspValTrpMetGlyAsnSerArgGlyAsnAla 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         137 TrpSerArgLysHisLysThrLeuSerIleAspGlnAspGluPheTrpAl 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53 eGlnHisGlnGlyTyrProCysGluGluTyrGluValAlaThrGluAspG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             aGlnLys11eLysMetTyrPheAlaLeuAlaProIleAlaThrValLysH
|::::::|||||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70 lyTyrIleLeuSerValAsnArgIleProArgGlyLeuValGlnProLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GlnGlyThrThrMetGlyPheIleAlaPheSerThrMetProGluLeuAl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   510 GAAACGGATCAAAACCTTCTATGCATTAGCTCCCGTTGCCACCGTGAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37 ProThriysAlaValAspProGluAlaPheMetAsnIleSerGluIleIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19 CCCACA......AACCCTGAAGTGACCATGAATATAAGTCAGATGAT
                                                                                                                                                                                                                                                                                                               Sequence 1528 BP; 392 A; 387 C; 329 G; 420 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                       Length: 372
Gaps: 3
Percent Identity: 56.452
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                                                                                                                                                                                                                                                                                                                                                                                       Quality: 1141.50
Ratio: 3.624
Percent Similarity: 84.677
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US-09-333-159-47 x AAT58915
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       55555555555555555<del>×</del>8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This is the nucleotide sequence encoding the dog pre-duodenal (i.e. gastric) lipase enzyme. The sequence can be used to generate transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dog; duodenal; gastric; lipase; transgenic; plant; recombinant; extra
food; absorption; fat; pancreatic; cystic fibrosis; exocrine; dairy;
hydrolysis; trans-esterification; substrate; enzyme; biofuel; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant human or canine pre-duodenal lipase prodn. in transgenic plants - useful for facilitating absorption of fat, as bio-catalysts and for prodn. of bio-fuel
                                                                                                                                                                                                                     1057 CACTTGGACTTTATCTGGGCCATGGATGCCCCTCAAGCGGTTTACAATGA 1106
                                                                                                                                                                                                                                                                                             352
                                                                                                                                           laPheAspTrpGlySerGluThrLysAsnLeuGluLysCysAsnGlnPro 335
                                                                             857 critigacigggaagcccagricagaacargargcacrarcarcagagc 906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lenee P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: /SIDS8/gcgdata/geneseq/geneseqn/NA1996.DAT:AAT58915
     807 TCAGAACGIGCICCACIGGICCCAGGCIGIIAAGICIGGGAAGIICCAAG
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                                                                                                                                                                                                                                                                                                                                                 HisvalAspPheIleTrpGlyLeuAspAlaProHisArgMetTyrAsnGl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
ID AAT58915 standard; cDNA to mRNA; 1528 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= a
/product= gastric lipase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers 1..1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dog gastric lipase coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F1g 1; 130pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BIOC-) BIOCEM SA.
(LJOU ) INST RECH JOUVEINAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     1107 AATTGTTTCCATGATG 1122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-OCT-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAT58915;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Merot B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Canis
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203

459

409

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16-DEC-1992;
                                                                                                                                                                    Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        153
  Canine gastric lipase; CGL; dog; fat; mucoviscidosis; enzyme; bloconversion; exocrine pancreatic insufficiency; ss.
                                                                                                                                                                                                                                                                                                                                                                                                      1006
                                                                                                                                                                                                                                                                                                                                                                                                                                       806
                                                                                                                                                                                                                                                                                                                                                                            352 pThrGlyGlyGlnAspTrpLeuSerAsnProGluAspValLysMetLeuL 369
isAlaLysSerProGlyThrLysPheLeuLeuLeuProAspMetMetile 236
                                                                                            269
                                                                                                                  706
                                                                                                                                           285
                                                                                                                                                                  756
                                                                                                                                                                                       MetSerArgAlaSerValTyrAlaAlaHisThrLeuAlaGlyThrSerVa 302
                                                                                                                                                                                                                                    319 laPheAspTrpGlySerGluThrLysAsnLeuGluLysCysAsnGlnPro 335
                                                                                                                                                                                                                                                                                                                                  352
                                                                                                                                                                                                                                                                                                                                             euSerGluValThrAsnLeuIleTyrHisLysAsnIleProGluTrpAla 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: /SIDS8/gcgdata/geneseq/geneseqn/NA1994.DAT:AAQ68389
                                             LysGlyLeuPheGlyLysGluPheLeuTyrGlnThrArgPheLeuAr
                                                                                                                                                                                                    386 HisValAspPhelleTrpGlyLeuAspAlaProHisArgMetTyrAsnGl
              560 ACACCGAAACCTGTTAAACAAACTCATGCTCGTCCCTTCGTTCCTCTTC
                                                                   610 AAGCTTATATTTGGAAACAAATATTC...TACCCACACCACTTCTTGA
                                                                                           gGln...LeuvalIleTyrLeuCysGlyGlnValIleLeuAspGlnIleC
                                                                                                            ysSerAsnIleMetLeuLeuLeuGlyGlyPheAsnThrAsnAsnMetAsn
                                                                                                                                                                GCAGCAACGCCCTGTTTATCATTTGTGGATTTGACACTTTGAACTTGAAC
                                                                                                                                                                                                                                                                                                                                 336 ThrProValArgTyrArgValArgAspMetThrValProThrAlaMetTr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualiflers
1..1143
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
ID AAQ68389 standard; DNA; 1531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93WO-FR01260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-FEB-1995 (first entry)
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AATTGTTTCCATGATG 1122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      uIleIleHisLeuMet 407
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                                                                                                                                        269
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sick patients (e.g. having altered levels of gastric lipase); to treat conditions associated with insufficiency (or lack) of lipases, esp. mucovisacidosis or exocrine pancreatic insufficiency and partic, where immobilised, for bioconversions, e.g. hydrolysis or transesterification (other mammalian gastric lipases, or derivs., can be used in this application).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGL is used to improve absorption of ingested fat, in healthy and
                                                                                                                                                                                                                                                                                                                                                                                                                The sequence given below is the sequence of figure 8, altered according to the amendments described on page 2 of the appended
                                                                                                                                                                                                                                                     #
                                                                                                                                                                                                                                       Recombinant canine gastric lipase and nucleic acid encoding are used for improving absorption of ingested fat, treating mucoviscidosis etc. and in enzymatic bio-conversions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CACCTACTGGGGATACCCAGCTGAGGAATATGAAGTTGTGACCGAAGACG 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       103 yAlaSe:AsnTrpIleSerAsnLeuProAsnAsnSerLeuGlyPheIleL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       euAlaAspAlaGlyPheAspValTrpMetGlyAsnSerArgGlyAsnAla 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TrpSerArgLysHisLysThrLeuSerIleAspGlnAspGluPheTrpAl 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       aPheSerTyrAspGluMetAlaArgPheAspLeuProAlaValIleAsnP 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       170 helleLauGlnLysThrGlyGlnGluLysIleTyrTyrValGlyTyrSer 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70 lyTyrileLeuSerValAsnArgileProArgGlyLeuValGlnProLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          113 GTTATARCCTTGGGATCGACAGAATTCCTTATGGGAGGAAAATTCAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53 eGlnH1:sGlnGlyTyrProCysGluGluTyrGluValAlaThrGluAspG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                313 TGGGCCAGGAGGAATCTGTACTACTCGCCCGACTCCGTCGAATTCTGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37 ProThrLysAlaValAspProGluAlaPheMetAsnIleSerGluIleIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22 CCCACA.....AACCCTGAAGTGACCATGAATATAAGTCAGATGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       263 TGGCCGACGCGGGTACGACGTGTGGCTGGGGAACAGCAGGGGGCAACACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1531 BP; 395 A; 386 C; 329 G; 421 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56.452
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Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to: 1531
                                                                                                         Junien J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to: AAQ68389 from: 1
                                                                                                                                                                                                                                                                                                                                                            2; Fig 8; 52pp; French.
                                                   (LJOU ) INST RECH JOUVEINAL
92FR-0015201
                                                                                                         Blanchard C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality: 1141.50
Ratio: 3.624
allamity: 84.677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-333-159-47 x AAQ68389
                                                                                                                                                                WPI; 1994-317890/26
                                                                                                                                                                                         P-PSDB; AAR56871.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                         Benicourt C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1
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203

413 187 563

253

269

Location/Qualifiers

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The inventors claim a DNA sequence encoding AAP60723 linked to a promoter upstream and a gene for a polypeptide downstream. Particular examples are the yeast emzyme AMG, the mammalian enzyme, gastric lipase and the mammalian lymphokine, interferon-alpha2.
                                                                                                                                                                                                                                                                                                                                                                    New precursor polypeptide of defined sequence - and corresp. DNA used to transform hosts for prodn. of the polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1367 BP; 397 A; 284 C; 269 G; 417 T; 0 other
                                                                                                                                                                                                                                                                                                                                                                                                                 Example; Fig 5; 60pp; English.
                                                                                                                                                                                        84GB-0032483.
85WO-GB00599.
86GB-0019568.
                                                                                                                                                             85WO-GB00599
                            47..103
/*tag= a
104..1243
/*tag= b
                                                                                                                                                                                                                                                  (BREW-) BREWING RES FOUND (TUBB/) TUBB R S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ratio: 3.416
Percent Similarity: 81.235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-09-333-159-47 x AAN60685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality: 1124.00
                                                                                                                                                                                                                                                                                                                        WPI; 1986-182910/28
                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAP60724
                                                                                                                                                                                        21-DEC-1984;
23-DEC-1985;
01-JAN-1986;
                                                                                                                                                             23-DEC-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
                                                                                                   WO860377E-A
                                sig_peptide
                                                        mat_peptide
                                                                                                                                 03-JUL-1586
                                                                                                                                                                                                                                                                                             Tubb RS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23
    PThrGlyGlyGlnAspTrpLeuSerAsnProGluAspValLysMetLeuL 369
                                                                                                                                562
                                                                                                                                                           236
                                                                                                                                                                                        612
                                                                                                                                                                                                                                                                                              660 TCAATTCTCGCCACCGAGGTATGCTCCCGCGAGACGGTGGATCTCCCTCT 709
                                                                                                                                                                                                                                                                                                                                                          302
                                                                                                                                                                                                                                                                                                                                                                                                                 302 IGlnAsnIleLeuHisTrpSerGlnAlaValAsnSerGlyGluLeuArgA 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         336 ThrProValArgTyrArgValArgAspMetThrValProThrAlaMetTr 352
               462
                                                                                                   aGlnLysIleLysMetTyrPheAlaLeuAlaProIleAlaThrValLysH 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  319 laPheAspTrpGlySerGluThrLysAsnLeuGluLysCysAsnGlnPro 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      910 ATGCCTCCCTACTACAACCTGACAGACATGCATGTGCCAATGGCAGTGTG 959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             369 euSerGluValThrAsnLeuIleTyrHisLysAsnIleProGluTrpAla 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: /SIDS8/gcgdata/geneseq/geneseqn/NA1986.DAT:AAN60685
                                                                                                                                                                          ACACCGAAACCCTGTTAAACTAAACTCATGCTCGTCCCTTCGTTCCTCTTC
220 18AlaLysSerProGlyThrLysPheLeuLeuLeuProAspMetMetIle
                                                                                                                                                                                                                                                                                                                                                                                                286 MetSerArgAlaSerValTyrAlaAlaHisThrLeuAlaGlyThrSerVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       386 HisvalaspPhelleTrpGlyLeuAspAlaProHisArgMetTyrAsnGl
                                          GlnGlyThrThrMetGlyPhelleAlaPheSerThrMetProGluLeuAl
                                                                                                                                                                                                                                                                                                                                      ysSerAsnIleMetLeuLeuLeuGlyGlyPheAsnThrAsnAsnMetAsn
                                                                                                                                                                                                                                                                             gGln...LeuValIleTyrLeuCysGlyGlnValIleLeuAspGlnIleC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
ID AAN60685 standard; DNA; 1367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-JUN-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1110 AATTGTTTCCATGATG 1125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ullelleHisLeuMet 407
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Length: 405 Gaps: 2 Percent Identity: 52.099

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106
                                                                                                             222
                                                                                                                                                                                                                                                                       273 AGAGACCTGTTGTGTTTTTGCAGCATGGTTTGCTTGCATCAGCCACAAAC 322
                                                                                                                                                                                                                                                                                                                                                                                             107 TrplleSerAsnLeuProAsnAsnSerLeuGlyPhelleLeuAlaAspAl 123
                               30
                                                           79
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                                                                                                                                                     26
                                                                                                                                                                                                                73
                             123 CIGGANGCCCTGAAGTGACTATGAACATTAGTCAGATGATTACTTATTGG
                                                                                                                                                                                                                           90 erArgProValValLeuLeuGlnHisGlyLeuValGlyGlyAlaSerAsn
                                                                                                                                                                                                             GlyTymProCysGluGluTyrGluValAlaThrGluAspGlyTyrIleLe
                                                                                        30 nValAsnSerValHisMetProThrLysAlaVal......
                                                           38 AGGTCCAAAATGTGGCTGCTTTTAACAATGGCAAGTTTGATA
Align seg 1/1 to: AAN60685 from: 1 to: 1367
```

Precursor polypeptide; secretion vector; enzyme; ss

Homo sapiens.

Sequence encoding pregastric lipase

AAN60685

1223 ATATCAGAAGATAAA 1237

323		372
123 373	aGlyPheaspValTrpMetGlyAsnSerArgGlyAsnAlaTrpSerArgL :::	140 422
140	ysHisLysThrLeuSerIleAspGlnAspGluPheTrpAlaPheSerTyr::::	156 . 472
157	AspGluMetAlaArgPheAspLeuProAlaValIleAsnPheIleLeuGl :::::	173 522
173 523	nLysThrGlyGlnGluLysIleTyrTyrValGlyTyrSerGlnGlyThrT	190
190 573	hrMetGlyPhellealaPheSerThrMetProGluLeualaGlnLysIle :::	206 . 622
207 623	LysMetTyrPhealaLeualaProIlealaThrValLysHisAlaLysSe	223 672
223 673	<pre>rProGlyThrLysPheLeuLeuLeuProAspMetMetIleLysGlyLeuP ::: :: ::: ::: CCTTATAAACAAACTTAGATTTGTTCCTCAATCCCTCTTCAAGTTATAT</pre>	240 722
240	heGlyLysLysGluPheLeuTyrGlnThrargPheLeuArgGlnLeuVal ::: ::	256 772
257	<pre>ileTyrLeuCysGlyGlnValileLeuAspGlnIleCysSerAsnileMe</pre>	273 · · · · · · · · · · · · · · · · · · ·
273 823	<pre>tLeuLeuLeuGlyGlyPheAsnThrAsnAsnMetAsnMetSerArgAlaS ::::::: </pre>	290 872
290 873	erValfyralaalaHisThrLeualaGlyThrSerValGlnAsnIleLeu 	306 922
307 923	HistrpSerGlnAlaValAsnSerGlyGluLeuArgAlaPheAspTrpGl :::	323 972
323 973	ySerGluThrLysAsnLeuGluLysCysAsnGlnProThrProValargT ::::: AAGCCCAGTTCAGAATAGGATGCACTATGATCAGTCCCCAACCTCCCTACT	340 1022
340 023	yrargValargAspMetThrValProThralaMetTrpThrGlyGlyGln ::: :::	356 1072
357 073	ASPIPLeuSerAsnProGluAspValLysMetLeuLeuSerGluValTh	373 1122
373 123	.rasnleuileTyrHisLysasnileProGluTrpalaHisValaspPhei 	390 1172
390 173	letrpGlyLeuAspAlaProHisArgMettyrAsnGluIleIleHisLeu :::::: :::::::: :::	406 1222
407	MetGlnGlnGluglu 411	

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The inventors claim a pregastric lipase protein and a gene encoding it. Gastric lipase protein is useful for oral administration to treat lipase deficiency, e.g. cystic fibrosis or pancreatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New gastric lipase protein, esp. of human origin - for treating lipase deficiency, and DNA sequences coding for it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80 ......rcrgtactggggactacatggttgttggaaattacatc 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30 nValAsnSerValHisMetProThrLysAlaVal......41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42 .....AspProGluAlaPheMetAsnIleSerGluIleIleGlnHisGln 56 :::|||||||||:::||||| :::
seq_name: /SIDS8/gcgdata/geneseq/geneseqn/NA1986.DAT:AAN60566
                                                                                                                                     Cystic fibrosis therapy; enzyme; lipase deficiency; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1367 BP; 397 A; 284 C; 269 G; 417 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps: 2
Percent Identity: 52.099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: AAN60566 from: 1 to: 1367
                                                                                                              Sequence encoding human pregastric lipase.
                                                                                                                                                                                    Location/Qualiflers
47.103
/*tag- a
104.1243
/*tag- b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 3; 39pp; English.
                        seq_documentation_block:
ID AAN60566 standard; DNA; 1367 BP.
                                                                                                                                                                                                                                                                                                                                    84GB-0021210.
85WO-GB00364.
86GB-0008897.
                                                                                                                                                                                                                                                                                                              85WO-GB00364
                                                                                      (first entry)
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Quality: 1124.00
Ratio: 3.416
Percent Similarity: 81.235
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US-09-333-159-47 x AAN60566
                                                                                                                                                                                                                                                                                                                                                                                     (CELL-) CELLTECH LTD. (LOWE/) LOWE P A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1986-081634/12.
P-PSDB; AAP60658.
                                                                                                                                                                                                                                                                                                                                   21-AUG-1984;
15-AUG-1985;
01-JAN-1986;
                                                                                    22-AUG-1991
                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                              15-AUG-1985;
                                                                                                                                                                                                                                                              WO8601532-A.
                                                                                                                                                                                                                                                                                     13-MAR-1986.
                                                                                                                                                                                                                           mat_peptide
                                                            AAN60566;
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us-09-333-159-47.p2n.rng

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aGlyPheAspValTrpMetGlyAsnSerArgGlyÁsnAlaTrpSerArgL 140
|||||:::|||||||||:::||||
TGGTTATGATGTGTGGCTGGGCAACAGCAGAGGAAACACCTGGGCCAGAA 422
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AGAGACCTGTTGTGTTTTTGCAGCATGGTTTGCTTGCATCAGCCACAAAC
                                                                                                         223 TGAAGTCAATAGAATTCCTTATGGGAAGAAAAATTCAGGGAATACAGGCC
                                                                                                                                                                                                                                423 GAAACTIGTACTATTCACCAGATTCAGTTGAATTCTGGGCTTTCAGCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LysMetTyrPheAlaLeuAlaProIleAlaThrValLysHisAlaLysSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         340 yrArgValArgAspMetThrValProThrAlaMetTrpThrGlyGlyGln
123 CTGGAAGCCCTGAAGTGACTATGAACATTAGTCAGATGATTACTTATTGG
                            GlyTyrProCysGluGluTyrGluValAlaThrGluAspGlyTyrIleLe
                                                                                                                                                                                                                                                                                                                                        ysHisLysThrLeuSerIleAspGlnAspGluPheTrpAlaPheSerTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                   GATGAAATGGCTAAATATGACCTTCCAGCCACAATCGACTTCATTGTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nLysThrGlyGlnGluLysIleTyrTyrValGlyTyrSerGlnGlyThrT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAAAACTGGACAGAAGCAGCTACACTATGTTGGCCATTCCCAGGGCACCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             257 IleTyrLeuCysGlyGlnValIleLeuAspGlnIleCysSerAsnIleMe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         323 ySerGluThrLysAsnLeuGluLysCysAsnGlnProThrProValArgT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      973 AAGCCCAGTTCAGAATAGGATGCACTATGATCAGTCCCAACCTCCCTACT
                                                           GGATACCCAAATGAAGATATGAAGTTGTGACTGAAGATGGTTATATTCT
                                                                                       uSerValAsnArgIleProArgGlyLeuValGlnProLysLysThrGlyS
                                                                                                                                                                                                               Trp11eSerAsnLeuProAsnAsnSerLeuGlyPheIleLeuAlaAspAl
                                                                                                                                                                                                                                                                                                                                                                                                     AspGluMetAlaArgPheAspLeuProAlaValIleAsnPheIleLeuGl
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This is the nucleotide sequence encoding the human pre-duodenal (1.e. plants) il pass enzyme. The sequence can be used to generate transgenic plants producing recombinant lipase in an enzymatically active form. Alternatively bases encoding amino acids 20-23 or 20-73 (1-4 or 1-54 of the mature protein, respectively) can be deleted to form the derivatives designated delta-4 or delta-54 respectively. Plants, or their extracts, expressing the lipases or the truncated derivatives, can be used:
                                                                                                                                                                                                                                                                                                                                                                         Duodenal; gastric; lipase; transgenic; plant; recombinant; extract; ss; food; absorption; fat; pancreatic; cystic fibrosis; exocrine; dairy; hydrolysis; trans-esterification; substrate; enzyme; blofuel; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant human or canine pre-duodenal lipase prodn. in transgenic plants - useful for facilitating absorption of fat, as bio-catalysts and for prodn. of bio-fuel
               390 leTrpGlyLeuAspAlaProHisArgMetTyrAsnGluIleIleHisLeu 406
                                                                                                                                                                                                                      seq_name: /SIDS8/gcgdata/geneseq/geneseqn/NA1996.DAT:AAT58916
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AspTrpLeuSerAsnProGluAspValLysMetLeuLeuSerGluValTh
                                                     373 rAsnLeuIleTyrHisLysAsnIleProGluTrpAlaHisValAspPheI
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Merot B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human gastric lipase coding sequence.
                                                                                                                                                                                                                                                                 BP.
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                                                                                                                                                                                                                                                 seq_documentation_block:
ID AAT58916 standard; DNA; 1367
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(LJOU ) INST RECH JOUVEINAL.
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                                                                                                                                                                                         1223 ATATCAGAAGATAAA 1237
                                                                                                                                                               407 MetGlnGlnGluGlu 411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sig_peptide
                                                                                                                                                                                                                                                                                            AAT58916;
357
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allergy; t.issue growth; regeneration; wound healing; burn; tumour; periodontal disease; thrombolytic condition; haemostatic condition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; hydrophobic domain; immune deficiency; autoimmune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ySerGluThrLysAsnLeuGluLysCysAsnGlnProThrProValArgT. 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: /SIDS8/gcgdata/geneseq/geneseqn/NA2001.DAT:AAF28689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ||:::||| ACAATGTGAATGTACCAATTGCAGTGTGGAACGTGGCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GACCTGTTGGCTGACCCCCAAGATGTTGGCTTTTGCTTCCAAAACTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1173 TCTGGGCAATGGATGCCCCTCAAGAAGTTTACAATGACATTGTTTCTATG
          523 AAAACCITCTATGCTCTAGCTCCTGTTGCCACTGTGAAGTATACAAAAG
                                                                          CTTATAAACAAACTTAGATTTGTTCCTCAATCCCTCTTCAAGTTTATAT
                                                                                                                           heGlyLysLysGluPheLeuTyrGlnThrArgPheLeuArgGlnLeuVal
                                                                                                                                                                                                       257 IleTyrLeuCysGlyGlnValIleLeuAspGlnIleCysSerAsnIleMe
                                                                                                                                                                                                                                    ACTGAAGTGTGCTCCCGTGAGATGCTGAATCTCCTTTGCAGCAATGCCTT
                                                                                                                                                                                                                                                                                     tLeuLeuLeuGlyGlyPheAsnThrAsnAsnMetAsnMetSerArgAlaS
                                                                                                                                                                                                                                                                                                                        ATTTATAATTTGTGGATTTGACAGTAAGAACTTTAACACGAGTCGCTTGG
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                                                 rProGlyThrLysPheLeuLeuProAspMetMetIleLysGlyLeuP
                                                                                                                                                      TIGGIGACAAAATAITCTACCCACACATCTTTGATCAATTCTTGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
ID AAF28689 standard; cDNA; 1308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (a) as pharmaceuticals or food to facilitate absorption of fat, either in healthy subjects or in patients with inadequate levels of gastric/pancreatic lipase e.g. thoses with cystic fibrosis or exocrine pancreatic insufficient, in the elderly or in patients undergoing medical treatment which alters fat adsorption; (b) for performing industrial or agricultural reactions, e.g. in processing of fats or in the dairy industry, for hydrolysis or transesterification reactions, etc., where the plant material may provide both enzyme and substrate. The transgenic plants can also be used for blofuel production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .....TCTGTACTGGGGACTACACATGGTTTGTTTGGAAAATTACATC 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   523 GAAAACTGGACAGAAGCAGCTACACTATGTTGGCCATTCCCAGGGCACCA 572
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 ArgMetGluMetTrpLeuLeuIleLeuValAlaTyrMetPheGlnArgAs 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .... AspProGluAlaPheMetAsnIleSerGluIleIleGlnHisGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GlyTyrProCysGluGluTyrGluValAlaThrGluAspGlyTyrIleLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AspGluMetAlaArgPheAspLeuProAlaValIleAsnPheIleLeuGl
                                                                                                                                                                                                     Sequence 1367 BP; 397 A; 284 C; 269 G; 417 T; 0.other;
                                                                                                                                                                                                                                                                                 Length: 405
Gaps: 2
Percent Identity: 52.099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38 AGGTCCAAAATGTGGCTGCTTTTAACAATGGCAAGTTTGATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30 nValAsnSerValHisMetProThrLysAlaVal....
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                                                                                                                                                                                                                                                                                                    3.416
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US-09-333-159-47 x AAT58916
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                                                                                                                                                                                                                                                                                                        Ratio:
                                                                                                                                                                                                                                                                 alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1
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1072

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772 273 306 922 323 1172

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1222

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AGTAACTGGATTTGCAACCTGCCCAACAACAGTTTGGCTTTCCTTCTGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAF28679;
                                                                                                         138
                                                                                                                                                                                 155
                                                                                                                                                                                                                                                          171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to human proteins (AAB6160B-AAB61617) and their coding sequences (AAF28679-AAF2869B). The proteins of the present invention have hydrophobic domains and can be used for the treatment of various immune deficiencies and disorders, such as severe combined immunodeficiency (SCID), multiple sclerosis, rheumatoid arthritis, autoimmune pulmonary inflammation, graft-versus-host disease and cullian-Barre syndrome. The proteins may also be useful in the treatment of allergic reactions and conditions, such as asthma and in regulation of haematopolesis or lymphoid cell deficiencies. The proteins may also have tissue growth or regeneration as well as wound healing and in the treatment of burns. The proteins may be used in the treatment of periodorial disease and in other tooth repair processes. Other uses include treatment of thrombolytic and haemostatic conditions, treatment of corprevention of tumours and inhibiting infection by bacteria, viruses,
                                                                                                                                                                                              New human proteins with hydrophobic domains, useful for the treatment of immune disorders, tumors, allergic conditions, thrombosis and microbial infection -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SerAsnTrp1leSerAsnLeuProAsnAsnSerLeuGlyPheIleLeuAl 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67 AGATCCCAAATGTGGCAGCTTTTAGCAGCAGCATGCTGGATGCTTCTTCT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          196 TACTGGGGTTATCCTTATGAAGAGTATGATGTTACAACAAAAGATGGTTA 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ......TyrMetPheGlnArgAsnValAsnSerValH1sMetProT 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38 hrLysAlaValAspProGluAlaPheMetAsnIleSerGluIleIleGln 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HisGlnGlyTyrProCysGluGluTyrGluValAlaThrGluAspGlyTy 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rlleLeuSerValAsnArgIleProArgGlyLeuValGlnProLysLysT 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14 ArgMetGluMetTrpLeuLeuIleLeuValAla.............
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1308 BP; 402 A; 246 C; 264 G; 396 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Identity: 56.223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to: 1308
                                                                                                                                                                                                                                                                         Claim 4; Pages 122-124; 153pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from: 1
                                             SAGAMI CHEM RES CENT.
PROTEGENE INC.
               99JP-0188835
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3.717
80.258
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US-09-333-159-47 x AAF28689
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                                                                                                                                         WPI; 2001-071581/08
                                                                                                     Kimura T;
                                                                                                                                                          P-PSDB; AAB61608
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             02-JUL-1999;
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                                                 (SAGA)
                                                                                                       Kato S,
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The present invention relates to human proteins (AAB61608-AAB61617) and their coding sequences (AAF28679-AAF28698). The proteins of the present invention have hydrophobic domains and can be used for the treatment of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; hydrophobic domain; immune deficiency; autoimmune disorder;
allergy; tissue growth; regeneration; wound healing; burn; tumour;
periodontal disease; thrombolytic condition; haemostatic condition;
                                                                                                                                                                                                                                                                                                                            545
                                                                                                                                                                                                                                                                                                                                                                                                                                                            595
                                                                                                                                                                                            495
                                                                                                                            erArglysHisLysThrLeuSerIleAspGlnAspGluPheTrpAlaPhe 154
                                                                                                                                                                                                                                                            SerTyrAspGluMetAlaArgPheAspLeuProAlaValIleAsnPheIl 171
                                                                                                                                                                                                                                                                                                                                                                                            eLeuGlnLysThrGlyGlnGluLysIleTyrTyrValGlyTyrSerGlnG 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        188 lyThrThrMetGlyPheIleAlaPheSerThrMetProGluLeuAlaGln 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        596 GCACCACCATAGCTTTTATAGCATTTTCTACAAACCCAGAACTGGCTAAA 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            205 LysIleLysMetTyrPheAlaLeuAlaProIleAlaThrValLysHisAl 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     646 AAGATTAAGATATTTTTGCACTGGCTCCAGTTGTCACAGTTAAATACAC 695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        221 aLysSerProGlyThrLysPheLeuLeuLeuProAspMetMetIleLys 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  696 CCAAAGTCCTATGAAAAACTAACAACCCTTTCCAGGCGAGTAGTTAAG 744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: /SIDS8/gcgdata/geneseq/geneseqn/NA2001.DAT:AAF28679
121 aAspAlaGlyPheAspValTrpMetGlyAsnSerArgGlyAsnAlaTrpS
                                                                                                                                                                        396 AGATAGTGGTTATGACGTGTGGTTGGGGAACACCCGAGGAAACACTTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human protein HP03372 coding sequence #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 3; Rage 113; 153pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
ID AAF28679 standard; cDNA; 699 BP
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(PROT-) PROTEGENE INC.
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P-PSDB; AAB61608.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200102563-A2
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immunodeficiency (SCID), multiple sclenois, theumatoid arthitis, autoimmune pulmonary inflammation, graft versus-host disease and guillain-barre syndrome. The proteins may also be useful in the treatment of allergic reactions and conditions, such as asthma and in regulation of haematopolesis or lymphoid cell deficiencies. The proteins may also have utility in compositions used for bone, cartilage, tendon and/or nerve tissue growth or regeneration as well as wound healing and in the periodontal disease and in other tooth repair processes. Other uses include treatment of thrombolytic and haemostatic conditions, treatment of prevention of tumours and inhibiting infection by bacteria, viruses,
    such as severe combined
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          307 GCTTTCCTTCTGGCAGATAGTGGTTATGACGTGTGGGTTGGGGAACAGCCG 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           200 roGluLeualaGlnLysIleLysMetTyrPhealaLeualaProIleala 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83 1GlnProLysLysThrGlySerArgProValValLeuLeuGlnHisGlyL 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              euValGlyGlyAlaSerAsnTrpIleSerAsnLeuProAsnAsnSerLeu 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GlyPheIleLeuAlaAspAlaGlyPheAspValTrpMetGlyAsnSerAr 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ValileAsnPheileLeuGlnLysThrGlyGlnGluLysileTyrTyrVa 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183 IGlyTyrSerGlnGlyThrThrMetGlyPheIleAlaPheSerThrMetP 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     257 TAATTGCATCTGCCAGTAACTGGATTTGCAACCTGCCCAACAACAGTTTG 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gGlyAsnAlaTrpSerArgLysH1sLysThrLeuSerIleAspGlnAspG 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   150 luPheTrpAlaPheSerTyrAspGluMetAlaArgPheAspLeuProAla 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       457 ACAATCAATTTATCATAGAGAAACTGGACAGAAGCGACTCTACTACGT 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18 TrpLeuLeuIleLeuValAla...TyrMetPheGlnArgAsnValAsnSe 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50 erGluIleIleGlnHisGlnGlyTyrProCysGluGluTyrGluValAla 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 ThrGluAspGlyTyrIleLeuSerValAsnArgIleProArgGlyLeuVa 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28 IGGAIGCIICTICIIGGAICTAIGIAIGGIIAIGACAAGAAAGGAAACAA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33 rValHisMetProThrLysAlaValAspProGluAlaPheMetAsnIleS
                                                                                                                                                                                                                                                                                                                    Sequence 699 BP; 216 A; 144 C; 148 G; 191 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps: 2
Percent Identity: 58.371
                                                                                                                                                                                                                                                                                                                                                                                                              Length:
    disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from: 1 to: 699
    immune deficiencies and
                                                                                                                                                                                                                                                                          fungi and other parasites.
                                                                                                                                                                                                                                                                                                                                                                                                         691.00
3.735
83.710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: AAF28679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
US-09-333-159-47 x AAF28679
                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
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expressed sequence tag; EST; probe; chemotactic; proliferative; thrombolutory; haematopoletic; chemotactic; analgasic; haemastatic; thrombolytic; antinflammatory; cytostatic; antibacterial; antifungal; antivital; antidabetic; antiasthmatic; vulnerary; antiparkinsonian; antivital; antidabetic; antiasthmatic; vulnerary; antiparkinsonian; antivital; autoimmune disordective; notropic; antiparkinsonian; vaccine; autoimmune disorder; multiple sclerosis; allergic condition; insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer; lymphoid cell deficiency; burn; osteoporosis; osteoarthritis; perform disorder; Alzheimmer's disease; stroke; parkinson's disease; Hutington's disease; coaqulation disorder; haemophilia; thrombosis; inflammatory disorder; Crohn's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      anticonvulsant; and antidepressant. The SESTS can be used for gene therapy and in vaccines. The SESTS are useful as probes for the identification and isolation of full-length cDNAs and genomic DNA molecules which correspond to the SESTS. Proteins encoded by the SESTs are useful in assays for determining biological activity and raising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAA43426 to AAA45925 represent specifically claimed secreted expressed sequence tags (SESTs), isolated from human, mouse, chicken and rat tissue sources. The SESTs can have a range of activities depending on the tissues they were isolated from. The activities include: chemotactic; proliferative; immunomodulatory; haematopoletic; chemotinetic; analgesic; haemostatic; thrombolytic; antihalammatory; ovytostatic; antibacterial; antifungal; antiviral; antidiabetic; antibacterial; antilucer; osteopathic; neuroprotective; nootropic; antiparkinsonian; antipsoriatic; cerebroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             expressed sequence tags (sESTs), useful for treating various disorders such as autoimmune, infectious, and central nervous system disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      proteins, comprising secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ن
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557 CAGAACT/3GCTAAAAAGATTAAGATATTTTTTGCACTGGCTCCAGTTGTC 606
                                           217 ThrValLysHisAlaLysSerProGlyThrLysPheLeuLeuLeuProAs 233
                                                                                   607 ACAGTTAAATACACCCAAAGTCCTATGAAAAACTAACAACCCTTTCCAG 656
                                                                                                                                                                                                                      seq_name: /SIDS8/gcgdata/geneseq/geneseqn/NA2000.DAT:AAA4349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chicken; rat, secreted expressed sequence
                                                                                                                                                                                                                                                                                                                                                                                                                        Human secreted expressed sequence tag SEQ ID NO:924.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tumour; infection; depression; psortasis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated polynucleotides, and encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LaVallie ER,
Bowman MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 441; 803pp; English.
                                                                                                                                                                                                                                                                  seq_documentation_block:
ID AAA44349 standard; cDNA; 617 BP.
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Treacy M,
                                                                                                                                                            657 GCGAGTASTTAAG 669
                                                                                                                                 233 pMetMetIleLys 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-317938/27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; mouse;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-OCT-1999;
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Merberg D,
                                                                                                                                                                                                                                                                                                                                   AAA44349;
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seq_documentation_block: ID AA234958 standard; cDNA; 1718 BP.

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antibodies. They may be useful for treatment of autoimmune disorders (multiple sclerosis, insulin dependent diabetes), allergic conditions (asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers, osteoporosis, osteoarthritis, central nervous system disorders (Alzheimer's, Parkinson's, Huntington's disease, stroke), coagulation disorders (haemophilia, thrombosis), inflammatory disorders (Crohn's psoriasis, tamours, bacterial, fungal or viral infections, depression and psoriasis, AAA45926 to AAA4591 represent linker variants which are given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            238.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    108
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.TCTGTACTGGGGACTACATGGTTTGGAAAATTACATCCTGGAA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCCAACCTGCCGAACAACAGCCTTGCCTTCATTCTGGCAGATGCTGGTTA 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 eAspValTrpMetGlyAsnSerArgGlyAsnAlaTrpSerArgLysHisL 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             142 ysThrLeuSerIleAspGlnAspGluPheTrpAlaPheSerTyrAspGlu 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    439 TGTACTATICACCAGATICAGTIGTGAATICTGGGCTTTTCAGCTTTGATGAA 488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 GluMetTrpLeuLeuIleLeuValAlaTyrMetPheGlnArgAsnValAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54 AAAATGTGGCTGCTTTTAACAATGGCAAGTTTGATA.......
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     389 TGATGTGTGGCTGGGCAACAGCAGGAAACACCTGGGCCAGAAGAAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32 nSerValHisMetProThrLysAlaVal......A
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                                                                                                                                                                                                        Sequence 617 BP; 181 A; 125 C; 139 G; 172 T; 0 other;
                                                                                                                                                                                                                                                                                                              Gaps: 2
Percent Identity: 60.526
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3.772
83.158
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US-09-333-159-47 x AAA44349
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Percent Similarity:
                                                                                                                                                                                                                                                                      alignment_scores:
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  888888888888888
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seq_name: /SIDS8/gcgdata/geneseq/geneseqn/NA2000.DAT:AA234958

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This is the nucleotide sequence of a contig assembled from the entire cDNA insert in clone ssl.pk0022.al and a portion of the cDNA insert in clone ssl.pk0022.al and a portion of the cDNA insert in clone sdp3c.pk004.n3 encoding the entire soybean cold triacylglycerol lipase (TAGL) (see AAV32309). The clones were isolated from soybean developing pod and seedling (5-10 day post germination) CDNA libraries. Novel acid and neutral TAGL polypeptides (5-10 day post centalpa, rice, soybean and wheat tissues are disclosed. The enzymes may be prepared recombinantly and used to raise antibodies, which may be prepared recombinantly and used to raise antibodies, which cell extracts. The polynucleotides may be used to create transgenic plants in which the TAGL levels are present at higher or lover levels than normal, or in cell types or developmental processes where they are not normally found. This would alter the level of triacylglycerol and choisereryl esters found in those cells. Accumulation of fatty acids with unusual structures may be desirable to eliminate expression of TAGL genes for certain applications. TAGL enzymes may also be used as targets to facilitate the processing of plant seed oils and for the development of novel seed oils. The TAGL enzymes can also be used as targets to facilitate the useful as herbicides. This is desirable because inhibition of the activity of elther of the enzymes could lead to an inhibition of plant primers, which are useful for genetic mapping, as markers for traits in the plymicleotides also serve as a source of probes and primers, which are useful for genetic mapping, as markers for traits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel plant triacylglycerol lipase polynucleotides used to alter the level of the enzyme in transgenic plants
                                                                                                                                              Iriacylgly:erol lipase; soybean; fatty acid; seed oil;
vegetable oil; transgenic plant; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1718 BP; 492 A; 353 C; 344 G; 529 T; 0 other
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Percent Identity: 32.634
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                                                                                                             triacylglycerol lipase cDNA
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                                                                                                                                                                                                                                           Location/Qualifiers
184..1416
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                                                                                                                                                                                                                                                                                                                                                                                              99WO-US09280.
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                                                                     (first entry)
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62.704
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P-PSDB; AAY32309.
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                                                                                                             Soybean acild
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                                                                       28-FEB-2001)
                                                                                                                                                                                                          Glycine max
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                                 AAZ34958;
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853
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCCTGCGGTGTTTAATTATGTGTTCAGCCAAACGGGGCAG...AAGATCA 712
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                                                                                                                                                                                                                                                                                                                                                          HisGlyLeuValGlyGlyAlaSerAsnTrpIleSerAsnLeuProAsnAs 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 yrTyrValGlyTyrSerGlnGlyThrThrMetGlyPheIleAlaPheSer 197
                                                                                 232 GICCIAACAACIGIGCCICGICAAGCACACGCIICAAGCCGIGGCAACII 281
                                                                                                                                                          49
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                                                                                                                                                                                                                                                                                                          alGlnProLysLysThrGlySerArg.....ProValValLeuLeuGln 97
                                                                                                                                                                                                                                                         aThrGluAspGlyTyrIleLeuSerValAsnArgIleProArgGlyLeuV 83
                                                          1 MetLeuGluThrLeuSerArgGlnTrpIleValSerHisArgMetGluMe 17
                                                                                                                       SerGluIleIleGlnHisGlnGlyTyrProCysGluGluTyrGluValAl
                                                                                                                                                                                                                                                                                                                                                                          euProAspMetMet......IleLysGlyLeuPheGlyLysLysGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          904 TITAAICCAAAAGGGITAGCIGIIGAIGCCITICICAAGICI.....
                                                                                                         17 tTrpLeuLeuIleLeuValAlaTyrMetPheGlnArgAsnValAsnSerV
                                                                                                                                                        34 alHisMetProThrLysAlaValAspProGluAlaPhe...MetAsnIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                      131 snSerArgGlyAsnAlaTrpSerArgLysHisLysThrLeuSerIleAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   257 eTyrLeuCysGlyGlnValIleLeuAspGlnIleCysSerAsnIleMetL
                                   to: 1718
                                   from: 1
                                   Align seg 1/1 to: AA234958
alignment_block:
US-09-333-159-47 x AA234958
                                                                                                                                282 A.....
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                             1133 GACCAGACTATAACATTATGCACTATGGAGAAATATTTCCTCCAATCTAT 1182
                                                                                                                                                                                                                                                                                                                                                                                                      1033 CTATICITGAIGAAIGAGCCICAGICAACAICAACAAGAACAIGGIGCA 1082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .....CTCAAGTTCCATGATGAGAACAAGCGCAGCGTTCAGTTCATC 1323
                                                                                                                                                                                 307 sTrpSerGlnAlaValAsnSerGlyGluLeuArgAlaPheAspTrpGlyS 324
                                                                                                                                                                                                                                                                             324 erGluThrLysAsnLeuGluLysCysAsnGlnProThrProValArgTyr 340
                                                                                                                                                                                                                                                                                                                                                                         355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               372 alThrAsnLeuIleTyrHisLysAsn.....Ile 381
274 euLeuLeuGlyGlyPheAsnThrAsnAsnMetAsnMetSerArgAlaSer 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              382 ProGluTrpAlaHisValAspPheIleTrpGlyLeuAspAlaProHisAr 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: /SIDSE/gcgdata/geneseq/geneseqn/NA2000.DAT:AAZ34956
                                                                                                                                                                                                                                                                                                                                                                       341 ArgValArgAspMet.....ThrValProThrAlaMetTrpThrGlyGl
                                                                                         ValTyrAlaAlaHisThrLeuAlaGlyThrSerValGlnAsnIleLeuHi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Triacylglycerol lipase; rice; fatty acid; seed oil; vegetable cil; transgenic plant; ss.
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32..1264
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ID AAZ34956 standard; cDNA; 1483 BP
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This is the nucleotide sequence of the CDNA insert in clone

Ilpase (TAGL) (see AAY23207). The clone was isolated from a rice

Ilpase (TAGL) (see AAY23207). The clone was isolated from a rice

leaf CDNA library. Novel acid and neutral TAGL polypeptides

(see AAY32301-17) and polynucleotides (see AAZ34950-66) from corn,

Catalpa, rice, soybean and wheat tissues are disclosed. The enzymes

may be prepared recombinantly and used to raise antibodies, which

are used for detecting the enzymes in situ in cells or in vitro in

cell axtracts. The polynucleotides may be used to create transgenic

plants in which the TAGL levels are present at higher or lower levels

than normal, or in cell types or developmental processes where they are

not normally found. This would alter the level of triacylajycerol and

cholesteryl esters found in those cells. Accumulation of fatty acids

with unusual structures may be desirable to eliminate expression of TAGL

foods. In addition, it may be desirable to eliminate expression of TAGL

genes for certain applications. TAGL enzymes may also be used to receive the

colls. The TAGL enzymes can also be used as targets to facilitate the

special as herbicides. This is desirable because inhibition of the

activity of either of the enzymes could lead to an inhibition of plant

proven. The polynucleotides also serve as a source of probes and

primers, which are useful for genetic mapping, as markers for traits

class and to isolate homologous sequences from other level of the enzyme in transgenic plants Claim 2; Page 44; 65pp; English spectes.

Sequence 1483 BP; 375 A; 334 C; 344 G; 430 T; 0 other;

Length: 365 Gaps: 13 Identity: 33.973 Percent 502.00 2.109 65.205 alignment_block: US-09-333-159-47 x AAZ34956 Quality: Ratio: Percent Similarity: alignment_scores

to: 1483 from: 1 Align seg 1/1 to: AA234956

89 GlyTyrProCysGluGluTyrGluValAlaThrGluAspGlyTyrIleLe uSerValAsnArgIleProArgGlyLeuValGln...ProLysLysThrG 57 73

89 lySerArgProValValLeuLeuGlnHisGlyLeuValGlyGlyAlaSer 105 GC.....CCTCCAGTTTTTCTTCAACATGGTCTTTTTCAGGGAGGAGAC 337

294

106 AsnTrpIleSerAsnLeuProAsnAsnSerLeuGlyPheIleLeuAlaAs 122 rgLysHisLysThrLeuSerIleAspGlnAspGluPheTrpAlaPheSer 155 139

122 pAlaGlyPheAspValTrpMetGlyAsnSerArgGlyAsnAlaTrpSerA 139

156 TyrAspGluMetAlaArgPheAspLeuProAlaValIleAsnPheIleLe 172 172 uGlnLysThrGlyGlnGluLysIleTyrTyrValGlyTyrSerGlnGlyT 189

1054 TGTTCAGCGTACTATCAGAGGCTGGGATCTACACCAGAACTTCTGTAC. 1153 1154 ATTGGTGACTATGGCCATATTGATTTGTTATGAGCGTGAAG 1195 364 pValLysMetLeuLeuSerGluVal.....ThrAsnLeuIleTyrH 378 364 857 ThrSerValGlnAsnIleLeuHisTrpSerGlnAlaValAsnSerGlyGl 316 316 uLeuArgAlaPheAspTrpGlySerGluThrLysAsnLeuGluLysCysA 333 snGlnProThrProValArgTyrArgValArgAspMet.....ThrVal 347 378 isLysAanileProGluTrpAlaHisValAspPheileTrpGlyLeuAsp 394LeuProA 233 233 spMetMetIleLysGlyLeuPheGlyLysLysGluPheLeuTyrGlnThr 249 858 GCTTCANTACATCAAGGATTGATTATTTTGGAGTATGAACCTCATCCA 907 GICATTIGCGICCICCGCATTIGACCIAAGCAGCATACCAGAATCACIG TGCT.....AGTTTTGTTCTCAGAGCAGTCGCCATGCATCTTGATC :::|||:::::|||::::|||
908 TCATCGACAAAAATCTGCACCATCTTTTCAGATGATGATGAAAGGCAC TACAGTCACA....CAGTCCAAAATTCTATATGTGGGGCATTCACAGGGAA hrThrMetGlyPheIleAlaPheSerThrMetProGluLeuAlaGlnLys 206 IleLysNetTyrPheAlaLeuAlaProIleAlaThrValLysHisAlaLy ATTAGCTCTGCAGCACTTCTTTGTCCTATTTCTTATCTTGATCATGTTAG 723 AGATGCTTGTT....ACTATGGGAATTCACCAGCTGAACTTCCGTAGC ArgPheLeuArgGlnLeuValIleTyrLeuCysGlyGlnValIleLeuAs 767 GACATGGGGGTTCAAATAGTAGATTCTTTGTGCGATGGTGAACACGTGGA pGlnIleCysSerAsnIleMetLeuLeuLeuGlyGlyPheAsnThrAsnA 283 snMetAsnMetSerArgAlaSerValTyrAlaAlaH1sThrLeuAlaGly ProThr.AlaMetTrpThrGlyGlyGlnAspTrpLeuSerAsnProGluAs GCGAAAGATGATGTTATGTGGACCTAATAAGATTTCTTAGGGAA 1240 395 AlaProHisArgMetTyrAsnGluIleIleHisLeuMetGlnGln 222 sSerProGlyThrLysPheLeuLeu 300 333 348 1055 1105 189 585 632 682 250

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82.50 109.43 176.52
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                                                                                                                                                                                                                                                                          seq_documentation_block:
    Sequence 2, Application US/08227108
    Fatert No. 5807726
    GENERAL INFORMATION:
    APPLICANT: Blanchard, Claufe
    APPLICANT: Benicourt, Claude
    APPLICANT: Junien, Jean-Louis
    TITLE OF INVENTION: Recombinant Dog Gastric Lipase
    NUMBER OF SEQUENCES: 21
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Pennie & Edmonds
    STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                    seq_name: /cgn2_6/ptodata/1/ina/5A_COMB.seq:US-08-227-108-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A.

ZIP: 10036
COMPUTER RADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/227,108
FILING DAFE: 03-APR-1994
CLASSIFICATION: 435
ATTONNEY/AGENT INFORMATION:
NAME: Fanucci, Allan A.
REGISTRATION NUMBER: 30,256
REFERENCE/DOCKET NUMBER: 7620-033
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELESA: 66141 PENNIE
TELEX: 66141 PENNIE
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TELEX: 66141 PENNIE
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Percent Identity: 56,452
                                                                                                                   /cgn2_6/ptodata/1/ina/5A_COMB.seq:US-08-348-891A-1 +
/cgn2_6/ptodata/1/ina/5A_COMB.seq:US-08-905-817-1 +
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/cgn2_6/ptodata/1/1na/6A_COMB.seq:US-08-683-838A-1
/cgn2_6/ptodata/1/1na/5B_COMB.seq:US-08-483-101-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
US-09-333-159-47 x US-08-227-108-2
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Percent Similarity: 84.677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: New York
STATE: New York
COUNTRY: U.S.A.
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; LOCATION:
US-08-227-108-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
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                                                                                                                                                                                                                                                                          -MODEL-frame+_p2n.model -DEV-x1p
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-Q-Cgn2_1/USPTO_spool/USO9333159/runat_31082001_122330_1399/app_query.fasta_1.488
-DB-Issued_Patents_na -QFPM-fastap -SUFFIX-p2n.rn1
-GAPOP-12.000 -GAPEXT-4.000 -MIRMATCH-0.100 -LOOPEL-0.000
-XGAPEXT-0.500 -GAPOP-6.000 -GGAPEXT-7.000 -YGAPOP-10.000
-XGAPEXT-0.500 -DELOP-6.000 -DELEXT-7.000 -YARPT-1
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-THR_SCORE-pct -THR_MAX-100 -THR_MIN-0 -ALIGN-15 -MODE-LOCAL
-USER-USO9333159_@CGN1_1_62 -NCFU-6 -ICPU-3 -LONGLOG -NO_XLPXY
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OM of: US-09-333-159-47 to: Issued_Patents_NA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database: Issued_Patents_NA:*
Database sequences: 324599
Latabase length: 9465562
Search time (sec): 69.100000
                                                                           Date: Sep 1, 2001 8:18 PM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query length: 423
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1007 TITCCAAGCICCCCAAICICAIITACCACAGGAAGAIICCICCIIACAAI 1056

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957 GAACGGIGGCAACGACTIGCIGGCCGACCCICACGAIGITGACCITITGC 1006
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yAlaSerAsnTrplleSerAsnLeuProAsnAsnSerLeuGlyPhelleL 120
                                                                                                                                                                                  eualaaspalaGlyPheaspValTrpMetGlyAsnSerArgGlyAsnAla 136
                                                                                                                                                                                                   260 TGGCCGACGCCGGGTACGACGTGTGGGGGAACAGCAGGGGCAACAC 309
                                                                                                                                                                                                                                                                           helleLeuGlnLysThrGlyGlnGluLysIleTyrTyrValGlyTyrSer 186
                                                                                                                                                                                                                                                                                                                                                                                                            GlnGlyThrThrMetGlyPheIleAlaPheSerThrMetProGluLeuAl 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         isAlaLysSerProGlyThrLysPheLeuLeuLeuProAspMetMetIle 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        237 LysGlyLeuPheGlyLysLysGluPheLeuTyrGlnThrArgPheLeuAr 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  302 lGlnAsnIleLeuHisTrpSerGlnAlaValAsnSerGlyGluLeuArgA 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 laPheAspTrpGlySerGluThrLysAsnLeuGluLysCysAsnGlnPro 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pThrGlyGlyGlnAspTrpLeuSerAsnProGluAspValLysMetLeuL 369
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                                                                                                                                               210 AGCCACAAACTGGATCTCCAACCTGCCCAACAACAGCCTGGCCTTCATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             253 gGln...LeuValIleTyrLeuCysGlyGlnValIleLeuAspGlnIleC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              857 CTTTTGACTGGGAAGCCCAGTTCAGAACATGATGCACTATCATCAGAGC
                                                  LysThrGlySerArgProValValLeuLeuGlnH1sGlyLeuValGlyGl
                                                                                160 AATATAGGCCGGAGACCTGTTGCATTTTTGCAACACGGTTTGCTCGCATC
                                                                                                                                                                                                                                                    TrpSerArgLysHisLysThrLeuSerIleAspGlnAspGluPheTrpAl
                                                                                                                                                                                                                                                                                                                       aPheSerTyrAspGluMetAlaArgPheAspLeuProAlaValIleAsnP
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37 ProThrIysAlaValAspProGluAlaPheMetAsnIleSerGluIleIl 53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 CCCACA......AACCCTGAAGTGACCATGAATATAAGTCAGATGAT
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                                                                                                                                                                      seq_name: /cgn2_6/ptodata/1/1na/5B_COMB.seq:US-09-073-674-2
                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Blanchard, Claure
APPLICANT: Benicourt, Claude
APPLICANT: Junien, Jean-Louis
TITLE OF INVENTION: Recombinant Dog Gastric Lipase
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Identity: 56.452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to: 1137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5072-D1-66-TMC
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                              eq_documentation_block:
Sequence 2, Application US/09073674
Patent No. 5958189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: CIISSEY, TODD M.
REGISTRATION NUMBER: 37,807
REFERENCE/DOCKET NUMBER: 50
TELECOMMUNICATION INFORMATION:
TELEPHONE: 734 622-7530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-333-159-47 x US-09-073-674-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                2800 Plymouth Road
Ann Arbor
                                                                                                                                                                                                                                                                                                                                                                                                                                   Warner-Lambert
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 1137 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                          1107 AATTGTTTCCATGATG 1122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                  402 ullelleHisLeuMet 407
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ZIP: .48105
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ratio: 3.624
Percent Similarity: 84.677
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Michigan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
STREET: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY:
; LOCATION:
US-09-073-674-2
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386
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357 GAACGGIGGCAACGACTIGCIGGCCGACCCTCACGAIGTIGACCTTIIGC 1006

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60 CACCTACTGGGGATACCCAGCTGAGGAATATGAAGTTGTGACCGAAGACG 109
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1007 TITCCAAGCICCCCAAICICATITACCACAGGAAGATICCICCITACAAI 1056
369 euSerGluValThrAsnLeuIleTyrHisLysAsnIleProGluTrpAla 385
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                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Junien, Jean-Louis
TITLE OF INVENTION: Recombinant Dog Gastric Lipase
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Identity: 56.452
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1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/227,108 FILING EATE: 03-APR-1994
                                                                                                                                                                                                                                                                                     seq_documentation_block:
    Sequence 4, Application US/08227108
    Patent No. 5807726
    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 7620
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELERA: 212 869-8864/9741
TELERA: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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Percent Similarity: 84.677
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US-08-227-108-4
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910 ATGCCTCCTACTACAACCTGACAGACATGCATGTGCCAATCGCAGTGTG 959
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1060 CACTTGGACTTTATCTGGGCCATGGATGCCCCTCAAGCGGTTACAATGA 1109
                                960 GAACGGIGGCAACGACTIGCIGGCCGACCCICACGAIGTIGACCTITIGC 1009
PThrGlyGlyGlnAspTrpLeuSerAsnProGluAspValLysMetLeuL 369
                                                                       369 euSerGluValThrAsnLeuIleTyrHisLysAsnIleProGluTrpAla
                                                                                                                                                     386 HisValAspPheIleTrpGlyLeuAspAlaProHisArgMetTyrAsnGl
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Percent Identity: 56.452
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,674
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    Sequence 4, Application US/09073674
    Patent No. 5998189
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Blanchard, Claire APPLICANT: Benicourt, Claude APPLICANT: Junien, Jean-Louis TITLE OF INVENTION: Recombinat NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: CLISSEY, TOOD M. REGISTRATION NUMBER: 37,807 REFERENCE/DOCKET NUMBER: 50 TELECOMMUNICATION INFORMATION: TELEPHONE: 734 622-7530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
US-09-333-159-47 x US-09-073-674-4
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nucleic acid
EDNESS: double
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|1110 AATTGTTTCCATGATG 1125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Ann Arbor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Michigan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
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; LOCATION:
US-09-073-674-4
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860 CITITGACTGGGGAAGCCCAGITCAGAACAIGAIGCACIAICAICAGAGC 909
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         660 TCAATITCTCGCCACCGAGGTATGCTCCCGCGAGACGGTGGATCTCCTCT 709
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                                                                                                                                                                                                                                                                                                                                                                                                                               euAlaAspAlaGlyPheAspValTrpMetGlyAsnSerArgGlyAsnAla 136
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TGGGCCAGGAGGAATCTGTACTACTCGCCCGACTCCGTCGAATTCTGGGC 362
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                                                      37 ProThrLysAlaValAspProGluAlaPheMetAsnIleSerGluIleIl
                                                                                                                              eGlnH1sGlnGlyTyrProCysGluGluTyrGluValAlaThrGluAspG
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                   to: 1140
                   from: 1
                 to: US-09-073-674-4
                   Align seg 1/1
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euSerGluValThrAsnLeuIleTyrHisLysAsnIleProGluTrpAla 385
                                                                             PThrGlyGlyGlnAspTrpLeuSerAsnProGluAspValLysMetLeuL 369
336 ThrProvalArgTyrArgValArgAspMetThrValProThrAlaMetTr 352
                                     910 ATGCCTCCCTACTACAACCTGACAGACATGCATGTGCCAATCGCAGTGTG
                                                                                                                                                                                                                                     HisvalaspPhalleTrpGlyLeuAspAlaProHisArgMetTyrAsnGl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Blanchard, Claire
APPLICANT: Benicourt, Claude
APPLICANT: Junien, Jean-Louis
TITLE OF INVENTION: Recombinant Dog Gastric Lipase
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT AFPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Fanucci, Allan A.
REGISTRATION NUMBER: 30,256
REFERENCE/DOCKET NUMBER: 76
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TELEPHONE: 212 790-9090
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID 0: 6:
SEQUENCE CHARACTERISTICS:
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|1110 AATTGTTTCCATGATG 1125
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Percent Similarity: 84.677
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FILING DATE: 03-APF
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                                                                       37 ProThrLysAlaValAspProGluAlaPheMetAsnIleSerGluIleIl
                                                                                                 19 CCCACA.....AACCCTGAAGTGACCATGAATATAAGTCAGATGAT
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                                     to: 1146
                                     from: 1
                                     to: US-08-227-108-6
US-09-333-159-47 x US-08-227-108-6
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pThrGlvGlyGlnAspTrpLeuSerAsnProGluAspValLysMetLeuL 369
                                                                                                                                                                                                            euSerGluValThrAsnLeuIleTyrHisLysAsnIleProGluTrpAla 385
                                                                                                                                                                                                                                                                                     386 HisValaspPheIleTrpGlyLeuAspAlaProHisArgMetTyrAsnGl
                                                    336 ThrProValArgTyrArgValArgAspMetThrValProThrAlaMetTr
                                                                                       907 ATGCCTCCCTACTACAACCTGACAGACATGCCATGTGCCAATCGCAGTGTG
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Percent Identity: 56.452
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,674
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Junien, Jean-Louis
TITLE OF INVENTION: Recombinant
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 eq_documentation_block:
Sequence 6, Application US/09073674
Patent No. 5998189
GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 5:
TELECOMMUNICATION INFORMATION
TELEPHONE: 734 622-7530
TELEFAX: 734 622-1553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2800 Plymouth Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Warner-Lambert
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                                                                                                                                                                                                                                                                                                                                                                  402 ullelleHisLeuMet 407
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Ratio: 3.624
ilarity: 84.677
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
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269 ysSerAsnIleMetLeuLeuLeuGlyGlyPheAsnThrAsnAsnMetAsn 285
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                                                                                                                                     19 CCCACA.....AACCCTGAAGTGACCATGAATATAAGTCAGATGAT
                                                                                                                                                                              53 eGlnHisGlnGlyTyrProCysGluGluTyrGluValAlaThrGluAspG
                                                                                                                                                                                                                                                               70 lyTyrIleLeuSerValAsnArgIleProArgGlyLeuValGlnProLys
                                                                                                 37 ProThrLysAlaValAspProGluAlaPheMetAsnIleSerGluIleIl
                                                           to: 1146
                                                         from: 1
                                                         Align seg 1/1 to: US-09-073-674-6
alignment_block:
US-09-333-159-47 x US-09-073-674-6
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euSerGluValThrAsnLeulleTyrHisLysAsnIleProGluTrpAla 385
                                                                                                              926
                                                                                                                                                    pThrGlyGlyGlnAspTrpLeuSerAsnProGluAspValLysMetLeuL 369
319 laPheAspTrpGlySerGluThrLysAsnLeuGluLysCysAsnGlnPro 335
                      336 ThrProValArgTyrArgValArgAspMetThrValProThrAlaMetTr
                                                                                              seq_name: /cgn2_6/ptodata/1/1na/5A_COMB.seq:US-08-227-108-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Blanchard, Claire
APPLICANT: Benicourt, Claude
APPLICANT: Junien, Jean-Louis
TITLE OF INVENTION: Recombinant Dog Gastric Lipase
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps: 3
Percent Identity: 56.452
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1155 Avenue of the Americas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
; Sequence 1, Application US/08227108
; Setent No. 5807726
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Fanucci, Allan A.
REGISTRATION NUMBER: 30,256
REFERENCE/DOCKET NUMBER: 76,
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US/0
FILING DATE: 03-APR-1994
CLASSIFICATION: 435
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| AATTGTTTCCATGATG 1122
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Ratio: 3.624
Percent Similarity: 84.677
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STATE: New York
COUNTRY: U.S.A.
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210 AGCCACAAACTGGATCTCCAACCTGCCCAACAACAGCCTGGCCTTCATCC 259
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                                                                                                                                        19 CCCACA.....AACCCTGAAGTGACCATGAATATAAGTCAGATGAT 59
                                                                                               137 TrpSerArgLy8HisLy8ThrLeuSerIleAspGlnAspGluPheTrpAl
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                                                             to: 1528
                                                           from: 1
                                                           Align seg 1/1 to: US-08-227-108-1
                   US-09-333-159-47 x US-08-227-108-1
alignment_block
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APPLICANT: Benicourt, Claude
APPLICANT: Junien, Jean-Louis
TITLE OF INVENTION: Recombinant Dog Gastric Lipase
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Warner-Lambert
STREET: 2800 "."
319 laPheAspTrpGlySerGluThrLysAsnLeuGluLysCysAsnGlnPro
                                                                                                         907 ATGCCTCCTACTACACCTGACAGACATGCCATGCGAGTGTG
                                                                                                                                                                                      euSerGiuValThrAsnLeuIleTyrHisLysAsnIleProGluTrpAla
                                                                                                                                                                                                                                                                                     1007 TITCCANGCICCCAAICICATITACCACAGGAAGAIICCICCTIACAAI
                                      857 CTTTTGACTGGGGAAGCCCAGTTCAGAACATGATGCACTATCATCAGAGC
                                                                               336 ThrProvalArgTyrArgValArgAspMetThrValProThrAlaMetTr
                                                                                                                                                                                                                                                                                                                                HisValAspPheIleTrpGlyLeuAspAlaProHisArgMetTyrAsnGl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM T'PE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
; Sequence 1, Application US/09073674
; Patent No. 5998189
; GENERAL INFORMATION:
APPLICANT: Blanchard, Claire
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Crissey, Todd M.
REGISTRATION NUMBER: 37,807
REFERENCE/POCKET NUMBER: 507
TELECOMMUNICATION INFORMATION:
TELEPHONE: 734 622-7530
TELEFAX: 734 622-1553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37,807
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 1528 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1107 AATTGTTTCCATGATG 1122
                                                                                                                                                                                                                                                                                                                                                                                                             402 ullelleHisLeuMet 407
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Ratio: 3.624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Ann Arbor
STATE: Michigan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , MOLECULE TYPE:
US-09-073-674:1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 48105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE
                                                                                                                                                                                                                                                369
                                                                                                                                                                                                                                                                                                                                386
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807 TCAGAACGTGCTCCACTGGTCCCAGGCTGTTAAGTCTGGGAAGTTCCAAG 856

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lGlnAsnIleLeuHisTrpSerGlnAlaValAsnSerGlyGluLeuArgA 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         137 TrpSerArgLysHisLysThrLeuSerIleAspGlnAspGluPheTrpAl 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      560 ACACCGAAACCTGTTAAACAAACTCATGCTCGTCCCTTCGTTCCTCTTC 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87 LysThrGlySerArgProValValLeuLeuGlnHisGlyLeuValGlyGl 103
                                                                                                                                                                                                                                                                                                                                                                                                                            160 AATATAGGCCGGGAGACCTGTTGCATTTTTGCAACACGGTTTGCTCGCATC 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       103 yAlaSerAsnTrpIleSerAsnLeuProAsnAsnSerLeuGlyPheIleL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          euAlaAspAlaGlyPheAspValTrpMetGlyAsnSerArgGlyAsnAla 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     260 TGGCCGACGCCGGGTACGACGTGTGGCTGGGGAACAGCAGGGGGCAACAC 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aPheSerTyrAspGluMetAlaArgPheAspLeuProAlaValIleAsnP 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           helleLeuGlnLysThrGlyGlnGluLysIleTyrTyrValGlyTyrSer 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          410 TCATCTTGAAGAAAACGGGACAGGACAAGCTACACTACGTTGGCCATTCC 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       aGlnLysIleLysMetTyrPheAlaLeuAlaProIleAlaThrValLysH 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                510 GAAACGGATCAAAACCTTCTATGCATTAGCTCCCGTTGCCACCGTGAAGT 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LysGlyLeuPheGlyLysLysGluPheLeuTyrGlnThrArgPheLeuAr 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            253 gGln...LeuValIleTyrLeuCysGlyGlnValIleLeuAspGlnIleC 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ysSerAsnIleMetLeuLeuLeuGlyGlyPheAsnThrAsnAsnMetAsn 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MetSerArgAlaSerValTyrAlaAlaHisThrLeuAlaGlyThrSerVa 302
                                                                                                                                                                                                                                                       60 CACCTACTGGGGATACCCAGCTGAGGAATATGAAGTTGTGACCGAAGACG 109
                                                                                                                                              53
                                                                                                                                                                                        29
                                                                                                                                                                                                                               70
                                                                                                                                                                                                                                                                                                                70 lyTyrIleLeuSerValAsnArgIleProArgGlyLeuValGlnProLys 86
                                                                                                                                                                                   19 CCCACA.....AACCCTGAAGTGACCATGAATATAAGTCAGATGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37 ProThrLysAlaValAspProGluAlaPheMetAsnIleSerGluIleIl
                                                                                                                                                                                                                               53 eGlnHisGlnGlyTyrProCysGluGluTyrGluValAlaThrGluAspG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATGAGTCGCTTGGATGTGTATCTGTCACATAATCCAGCAGGAACATCGGT
  Percent Identity: 56.452
                                                                                                       to: 1528
                                                                                                         from: 1
                                                                                                    to: US-09-073-674-1
                                       alignment_block:
US-09-333-159-47 x US-09-073-674-1
84.677
Percent Similarity:
                                                                                                    Align seg 1/1
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APPLICANT: COIE, Philip
APPLICANT: COIE, Thilip
APPLICANT: KULTYAN, JOHN
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
CURRENT APPLICATION NUMBER: US/09/356,952
CURRENT PILING DATE: 1999-07-19
EARLIER APPLICATION NUMBER: 60/093,631
EARLIER FILING DATE: 1998-07-21
NUMBER OF SEO ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14819 CTTGATACCAAATATAGAACGACAGATTCTGACAAGAAGAAGAGGGCCAC 14868
                                                                                                                                                                                                                                                                                                        957 GAACGETGGCAACGACTTGCTGGCCGACCTCACGATGTTGACCTTTTGC 1006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93 alValLeuLeuGlnHisGlyLeuValGlyGlyAlaSerAsnTrpIleSer 109
319 laPheAspTrpGlySerGluThrLysAsnLeuGluLysCysAsnGlnPro 335
                                                                                                                  PThrGlyGlyGlnAspTrpLeuSerAsnProGluAspValLysMetLeuL 369
                                                                                                                                                                                                                                                                           euSerGluValThrAsnLeuIleTyrHisLysAsnIleProGluTrpAla 385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: /cgn2_6/ptodata/1/ina/6A_COMB.seq:US-09-356-952-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 GluGluTyrGluValAlaThrGluAspGlyTyrIleLeuSerVal...As
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76 nArgileProArgGlyLeuValGlnProLysLysThrGlySerArgProV
                               336 ThrPrcValArgTyrArgValArgAspMetThrValProThrAlaMetTr
                                                                                                                                                                                                                                                                                                                                                                    386 HisValAspPheIleTrpGlyLeuAspAlaProHisArgMetTyrAsnGl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length: 376
Gaps: 16
Percent Identity: 25.532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
; Sequence 12, Application US/09356952;
; Patent No. 6i17663;
; GERERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: US-09-356-952-12
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US-09-333-159-47 x US-09-356-952-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Borlack-Sjodin, Ann
APPLICANT: Margarit, S. M.
APPLICANT: Bor-Sogi, Dafna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1107 AATTGTTTCCATGATG 1122
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1.263
57.181
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Ratio:
Percent Similarity:
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.....lleProGluTrpAlaHisValAspPheIleTrpGlyLeuAspAl 395

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15016 cGAAAGTACCGACACTAGCT........rccaGGTGGGACTGGGAC 15053
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15285 ....TTACTTAACGAGAAATTGTTTGTTAAGCTTATGACAAAGGAAATC 15329
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15421 TTTGTTACACCATCTTCAATTACCTGTTTGATTGGAACGATACCCTTTGG 15470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .......GTGGACGGAGAAA 15687
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                                                                                                                                                                                                                                                                                                                                                                                              156 TyrAspGluMetAlaArgPheAspLeuProAlaValIleAsnPheIleLe 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          172 uGlnLysThrGlyGlnGluLysIleTyrTyrValGlyTyrSerGlnGlyT 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       189 hrThrMetGlyPheIleAlaPhe......195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ......SerThrMetProGluLeuAlaGlnLysIleLysMetTyrPh 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   210 eAlaLeuAlaProIleAlaThrValLysHisAlaLysSerProGlyThrL 227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   285 AsnMetSerArgAlaSerValTyrAlaAlaHisThrLeuAlaGlyThrSe 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            351 .MetTrpThrGlyGlyGlnAspTrpLeuSerAsnProGluAspValLysM 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      268 leCysSerAsnIleMetLeuLeuLeuGlyGlyPheAsnThrAsnAsnMet
                                                    110 AsnLeuProAsnAsnSerLeuGlyPheIleLeuAlaAspAlaGlyPheAs
                                                                                                                                                                 126 pValTrpMetGlyAsnSerArgGlyAsn.....AlaTrpSerArg.
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APPLICANT: Gubbay, Johnathan
APPLICANT: Skinner, Michael
TITLE OF INVENTION: A cDNA Library Prepared during
TITLE OF INVENTION: Regression of Rat Prostate and Methods of Use Thereof
CORRESPONDENCE: 15
ADDRESSED: David A 12010
15738 TGGTACATTGATGAGTATGCCCATATTGATGTCCTATGGCACATGATGT 15787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                139 ArgLysHisLysThrLeuSerIleAspGlnAspGluPheTrpAlaPheSe 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  155 rTyrAspGluMetAlaArgPheAspLeuProAlaValIleAsnPheIleL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 AGGAAACATGTGCGCCTAGACCCAGATTCTAAAGAATTTTGGGATTTTAG
                                                                                                                                                  seq_name: /cgn2_6/ptodata/1/1na/5A_COMB.seq:US-08-751-782-2
                                                                                                                                                                                                                                                                                                                                                                                                                                 E: David A. Jackson, Esq.
411 Hackensack Ave, Continental Plaza, 4th
Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Identity: 56.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,782 FILING DÄTE: 18-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: US-08-751-782-2 from: 1 to: 178
                                                                                                       15788 CATAGAGAGATTGGTAAACCAATTTTA 15815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: JACKSON-ESQ., David A. REGISTRATION NUMBER: 26,742
RECISTRATION NUMBER: 600-1-190
TELECOMMUNICATION:
TELEPHONE: 201-487-5800
                                                           395 aProHisArgMetTyrAsnGluIleIle 404
                                                                                                                                                                                                            Sequence 2, Application US/08751782
Patent No. 5821352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-333-159-47 x US-08-751-782-2
                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Heintz, Nathaniel
APPLICANT: Gubbay, Johnathan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 178 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           155.00
3.780
82.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New Jersey
: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                              seq_documentation_block:
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Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07601
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.........CAGAAAAGAC 116
                                             85 ProLysLysThrGlySerArgProValValLeuLeuGlnHisGlyLeuVa 101
                    172 euGlnLysThrGlyGlnGluLysIleTyrTyrValGlyTyrSerGlnGly 188
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: LI, JOACHIM J
APPLICANT: LI, JOACHIM J
APPLICANT: GAVIN, Kimberly
TITLE OF INVENTION: ORIGIN OF REPLICATION COMPLEX GENES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT 4 Embarcadero Center, Suite 3400
                                                                                                        seq_name: /cgn2_6/ptodata/1/ina/5A_COMB.seq:US-08-484-105-21
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MEDIUM TYPE: PLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CNURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Osman Ph.D., Richard Aron
REGISTRATION NUMBER: 36,627
REELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-8770
TELEFAX: (415) 494-8771
TELEFAX: 910 27729
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                            Align seg 1/1 to: US-08-484-105-21
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US-09-333-159-47 x US-08-484-105-21
                                                                                                                                                                                                                                                                                                                                                                   LAURENSON, Patricia
HERSKOWITZ, Ira
                                                                                                                                                                                                                                                                                                        : RINE, Jasper
: FOSS, Margit
: MCNALLY, Francis J
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APPLICANT: BELL, Stephen P
APPLICANT: KOBAYASHI, Ryuji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1676 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality: 105.00
Ratio: 0.802
Percent Similarity: 47.122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
US-08-484-105-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Heintz, Nathaniel
APPLICANT: Gubbay, Johnathan
APPLICANT: Skinner, Michael
TITLE OF INVENTION: A cDNA Library Prepared during
TITLE OF INVENTION: Regression of Rat Prostate and Methods of Use Thereof
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              139 ArgLysHisLysThrLeuSerIleAspGlnAspGluPheTrpAlaPheSe 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                172 euGlnLysThrGlyGlnGluLysIleTyrTyrValGlyTyrSerGlnGly 188
                                                                                        155 rTyrAspGluMetAlaArgPheAspLeuProAlaValIleAsnPheIleL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 AGGAAACATGTGCGCTAGACCCAGATTCTAAAGAATTTTGGGATTTTAG 56
                                                                                                                                                   seq_name: /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-925-171-2
                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Identity: 56.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/925,171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: US-08-925-171-2 from: 1 to: 178
                                                                                                                                                                                                                Sequence 2, Application US/08925171
Patent No. 5928871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC-DOS/MS-
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US-09-333-159-47 x US-08-925-171-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 6
TELECOMMUNICATION INFORMATION
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 178 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  155.00
3.780
82.000
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                              documentation_block:
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Ratio:
Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
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COUNTRY:

alignment_scores:

US-08-925-171-2

CLONE

LAURENSON, Patricia , Margit LLY, Francis

MCNALLY,

KOBAYASHI, Ryuji

RINE, Jasper

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571 AGAGTGGATGCACGGAAAGATGGGCTCAATGTAAAAGTTCTTCTTGGAGC 620
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  681
                                         117 GAATGGAAAAGAGAATGCTTCTAGAAATTTGCAATCAAATTTAGAAGAAG 166
                                                                                                                                                                               124 GlyPheAspValTrp.....MetGlyAsnSer.....ArgGl 134
                                                                                                                                                                                                                                GCAATCGAAAATTACTTTATGCAAGGAAAATCGGCGTCAGAACGAATGAA 266
                                                                                                                                                                                                                                                                              134 yAsnAlaTrpSerArgLysHisLys......ThrLeuS 145
                                                                                                                                                                                                                                                                                                                                                                      145 erileAspGlnAspGluPheTrpAlaPheSerTyrAspGluMetAlaArg 161
                                                                                                                                                                                                                                                                                                                                                                                                      162 PheAspLeuProAlaValIleAsnPheIleLeuGlnLysThrGlyGlnGl 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .....TITAATATICTITIGCACGGTGTCGGTTCGAAGCGTGATG 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               292 yralaalaHisThrLeualaGlyThrSerValGlnAsnIleLeuHisTrp 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        262 GlnValIleLeuAspGlnIleCysSerAsnIleMetLeuLeuGlyGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              417 ATTCGAAAAACGATTGGAGCATCTCGCGGATAATGATTTCGGA.....
101 lGlyGlyAlaSerAsnTrpIleSerAsnLeuProAsnAsn.....
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85 ProLystysThrGlySerArgProValValLeuLeuGlnHisGlyLeuVa 101
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APPLICANT: HERSKOWITZ, Ira
APPLICANT: LI, Joachim J
APPLICANT: GAVIN, Kimberly
AITLE OF INVENTION: ORIGIN OF REPLICATION COMPLEX GENES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                          STREET: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT CITY: San Francisco Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101 1GlyGlyAlaSerAsnTrpIleSerAsnLeuProAsnAsn.....
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Gaps: 13
Percent Identity: 21.942
                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,106
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: OSman Ph.D., Richard Aron
REGISTRATION NUMBER: 36,627
REGISTRATION NUMBER: A-59032/DJB/RAO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from: 1
                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
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US-09-333-159-47 x US-08-484-106-21
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TELERAX: (415) 494-871
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 21
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1676 base pairs
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0.802
47.122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                     COUNTRY: USA
ZIP: 94111-4187
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US-08-484-106-21
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134

seq_name: /cgn2_6/ptodata/1/ina/5A_COMB.seq:US-08-484-106-21

Sequence 21, Application US/08484106 Patent No. 5614618

seq_documentation_block

GENERAL INFORMATION: APPLICANT: STILLMAN, Bruce APPLICANT: BELL, Stephen P

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245
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417 ATTCGAAAAACGATTGGAGCATCTCGGGATAATGATTTCGGA...... 459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         292 yralaalaHisThrLeuAlaGlyThrSerValGlnAsnIleLeuHisTrp 308
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yAsnAlaTrpSerArgLysHisLys.....ThrLeuS 145
                                                                                          161
                                                                                                                                                                                    162 PheaspLeuProAlaValIleAsnPheIleLeuGlnLysThrGlyGlnGl 178
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                                                                                          145 erIleAspGlnAspGluPheTrpAlaPheSerTyrAspGluMetAlaArg
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1: 4025 EXECUTIVE SQUARE, STE 1400
CALIFORNIA
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    Sequence 24, Application US/08602359A
    Patent No. 5942430
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APPLICANT: SWANSON, Ronald V.
APPLICANT: WARREN, Patrick V.
APPLICANT: KOSMOTKA, Anna
TITLE OF INVENTION: ESTERASES
NUMBER OF SEQUENCES: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: ROBERTSON, Daniel E.
APPLICANT: RURPHY, Dennis
APPLICANT: REID, John
APPLICANT: MAFFIA, Anthony
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
STREET: 42
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278 TTGCGCCG......GAGGGGCTCACCTACAAGAGTTCAGCGTG 315
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483 CITCCGGGGCCACGGGGGGGGCTCGACGACGATGGG...... 525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49 leSerGluIleIleGlnHisGlnGlyTyrProCysGluGluTyrGluVal
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Percent Identity: 22.778
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                                                                                                                                                                                                                                                                                                     09010/01060
                                                                                                                APPLICATION NUMBER: US/08/602,359A FILING DATE: February 16, 1996 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER:
                  MEDIUM TYPE: 3.5 INCH DISKETTE COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
US-09-333-159-47 x US-08-602-359A-24
                                                                                                                                                                                                                                                       NAME: HAILE, LISA A.
REGISTRAITON NUMBER: 38,347
REPRENCE/DOCKET NUMBER: 0901
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
                                                                        SOFTWARE: WORD PERFECT 6.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                           1041 NUCLEOTIDES
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COMPUTER READABLE FORM
                                                            OPERATING SYSTEM:
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Ratio:
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                                                                                                                                                                                                                    FILING DATE:
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to: US-08-232-519-1 from: 1 to: 1167

Align seg 1/1

148 InAspGluPheTrpAlaPheṢerTyrAspGluMetAlaArgPheAspLeu 164 :: :: 526CCCGGGAGGTGCTGGATGCC 546	
165 ProAlaValiteAsnPheileLeuGlnLysThrGlyGlnGluLysIleTy 181	
181 rTyrValGlyTyrSerGlnGlyThrThrMetGlyPheile 194 	
Seq_name: /cgn2_6/ptodata/1/1na/5A_COMB.seq:US-08-232-519-1	
<pre>seq_documentation_block:</pre>	
LICA	
Yagi, S	
PONDENCE ADDRESS:	
; STREET: 1251 Avenue of the Americas ; CITY: New York	
10020 READABLE FORM:	
ppy disk compatible	
1 DATA: SR: US/08/2	
CLASSIFICATION: 435	
APPLICATION NUMBER: JP 5-96286	
G DATE: Y/AGENT I	
; NAME: Haley Jr, James F ; REGISTRATION NUMBER: 27,794	
; REFERENCE/DOCKET NUMBER: SHGN-4; TELECOMMUNICATION INFORMATION:	
; TELEPHONE: (212) 596-9000 ; TELEFAX: (212) 596-9090	
; TELEX: 14-8367 ; INFORMATION FOR SEQ ID NO: 1:	
; SEQUENCE CHARACTERISTICS; ; LENGTH: 1167 base pairs	
; TYPE: nucleic acid ; STRANDEDNESS: double	
; TOPOLOGY: linear ; MOLECULE TYPE: DNA (genomic)	
SOURCE:	
STRAIN: ACC 12873	
; FEATURE: ; NAME/KEY: CDS ; LOCATION: 11164 HS-DR-222-510-1	•
alignment_scores: Quality: 98.50 Length: 400 Ratio: 0.518 Gaps: 20 Percent Similarity: 47.500 Percent Identity: 20.250	
alignment_block: ns-09-333-150-47 v ns-08-332-510-1	•
6TC-757-90-SD X	

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114 snSerLeuGlyPheIleLeuAlaAspAlaGlyPheAspValTrpMetGly 130
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                                      111:::
326 ATGCCTCTGCGGGGAACCCAAGCAGGTTACGGTAGGCGAACACACGCTA 375
                                                                                                                                                                                                                                                                                                          97 nHisGlyLeuValGlyGlyAlaSerAsnTrpIleSerAsnLeuProAsnA 114
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                                                                                                                                                                                 69 spGlyTyrIleLeuSerValAsnArgIleProArgGly.....LeuVal 83
                                                                                                                                                                                                                                                                             84 GlnProLysLysThrGlySerArg......ProValValLeuLeuGl 97
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38 ThrLysAlaValAspProGluAlaPheMetAsnIleSerGluIleIleGl
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910	910GGGCATCAGGCGGATGATCTGCACTCGGTGCTAGCTGGGGCG 951	951
325	325 GluthrLysAsnLeuGluLysCysAsnGlnProThrProValArgTyrAr 341	341
952	952 GAAACA	957
341	341. gValargaspMetThrValProThrAlaMetTrpThrGlyGlyGlnAspT 358	358
958		986
358	358 rpLeuSerAsnProGluAspValLysMetLeuLeuSerGluValThrAsn 374	374
989	989 AAATTCTTTTTGTCTCCCAGCCGCTGGCCTGCCTGCCAGATGTCATCCCCGTG 1038	1038
375	AsnileProGluTrpAl	389
1039	1039 ACAGTGTATGAAGAACAGGCCATCTGCCGCAGCTTGAACATGCAACAGA 1088	1088
389	389 elleTrpGlyLeuAspAlaProHisArgMetTyrAsnGlullelleHisL 406	406
1089	1089 TGTG	1108
406	406 euMetGlnGlnGluGluThrAsnLeuSerGlnGlyArgCysGluAla 421	421
1109		1158

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musculus adul
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Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itch, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shibata, K., Itoh, M., Alzawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Kithuchi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Yamamoto, R., Watsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watshika, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Okazaki, Y., Muramatsu, M., Inoue, Y. and Hayashizaki, Y. Rikin integrated sequence analysis (RISA) system -- 384 format Genome Res. 10 (11), 1757-1771 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                             AK019504 2927 bp mRNA HTC 08-FEB-2001 Mus musculus 0 day neonate skin cDNA, RIKEN full-length enriched Library, clone:4632427C23, full insert sequence.

AKC19504 GI:12859754
                                                                                                                                                                                                                                                                                                                                                CAF trapper.
Mus musculus (strain:C57BL/6J) 0 day neonate skin cDNA to mRNA, clone_lib.RIKEN full-length enriched mouse cDNA library clone-4633427C23.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The RIKEN Genome Exploration Research Group Phase II Team and FANTOM Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5 (bases 1 to 2927)
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URi:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
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High-efficiency full-length cDNA cloning
Methods Enzymol. 303, 19-44 (1999)
3.4e-120
4.8e-120
2.4e-117
4.7e-116
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2318.87
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2247.21
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gb_htc:AK009923
gb_htc:AK010091
gb_htc:AK010110
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VERSION
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SOURCE
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AUTHORS
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Query: US-09-333-159-47
Query length: 423
Database: EST:*
Database sequences: 10228115
Database length: 431459454
Search time (sec): 1357.660000
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                                                                                                      About: Results were produced by Copyright (c) 1993-2000
  of: US-09-333-159-47 to:
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GGTTAAAGGAAGGATCCAGGCCAGTGGTGTTACTGCAACATGGTCTT ValGlyGlydlyalaSerAsnTrplleSerAsnLeuProAsnAsnSerLeuGl :::	151 Phetrphlaphe	CATGCCCTGAAGCACTGGGTAAAGAATTGTGACTTGTGGTATTTGGATTG 7	154 154 703 CTGTGTAGTTCCCAACTCAATAACCCCCAAGTTTTCTTATTATCCTGTGC 752	TGATGT:GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	803 GGTTGAAAACAGTGTCTGGTGATGAGAATGGAGTGGGAAAGG 852	853 TATCCASTCATTTCCGTGTGAGTATGTAGGATTAACTCCCTCGTAT 902	903 AGGACAACAGGACTGCCACCCCCAAGACATGAGACCAAGGTGTCATTAAAT 952 154	GCTTTACTCAAGTTCCTAATGTCCTTACTAACCACTGATGGTCAACCTGT	TCTCTATGCATTTGGTCAGATATGAGTTTTGTTACCATTCATCCTGCAAA 1	GAAATCTGCATACCCCTGAGCTGTTTTAGTTGCAGGGTAGGACATGCTTC 1	ACATCAGCAGTTGGGTGAGTTTAAAACTTCTCAATAACCATTACTAT 1	AGTACAGCATCCAGAGAATAGACATTTCTCAGGTTTGAAACAAATCCG	TCTCAAGGATTTTGAGGAACACGGTGACAAACTAACAACACTGACACTGG	1303 TCGGGGGGATTTTJGTTAGCAGATCTGGGGGATTTGACTTGTTT 1352
	FEATURES LOCATION/Qualiflers Location/Qualiflers 12927 /organism="Mus musculus" /strain="C57BL/65"	633	/Clone_lib="KikkN full-length enriched mouse cDNA library" /dev_stage="0 day neonate" 153662 153662 //orde="pluative"	/profein_id="BAB31766.1" /profein_id="BAB31766.1" /db_xref="G1:12859755" /translation="MSFILSRWWTVSHRVEIWLLILVAYLLQRNVNSGHLPTKAADPE AFMNVSEIIKHKGYPSEEYEVATEDGYILSVNRIPRGQTRLKKEGSRPVVLQHGLLG DASWHISNLPNNSLGFILADGFDVWMONSRGWTWSRHKTLSTOODEFFARRYKNTL	RVEVDIDMP" al 29082913 .note-"putative"	POLYA_SILE 292/ BASE COUNT 837 a 581 c 664 g 845 t ORIGIN	alignment_scores: Quality: 1836.00 Length: 682 Ratio: 4.567 Gaps: 2 Percent Similarity: 58.944 Percent Identity: 54.106	alignment_block: US-09-333-159-47 x AK019504 Align seg 1/1 to: AK019504 from: 1 to: 2927	1 MetLeuGluThrLeuSerargGlnTrpIleValSerHisargMetGluMe 17 	17 tTrpLeuLeulleLeuValalaTyrMetPheGlnargasnValasnSerV 34 :	34 alHisMetProThrLysAlaValAspProGluAlaPheMetAsnIleSer 50	51 GluileileGlnHisGlnGlyTyrProCysGluGluTyrGluValAlath 67 ::: :::	67 rGluaspGlyTyrIleLeuSerValasnarglleProArgGlyLeuValG 84 	84 lnProLysLysThrGlySerArgProValValLeuGlnHisGlyLeu 100 ::

mRNA,

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2 (sites)
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itch,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected CDNAs to
prepare full-length CDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                    tongue cDNA, RIKEN full-length enriched 8, full insert sequence.
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The RIKEN Genome Exploration Research Group Phase II Team and
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Nature 409, 685-690 (2001)
5 (bases 1 to 1349)
                                                                                                                                                                  CAP trapper.

Mus musculus (strain:C57BL/6J) adult male tongue cDNA to clone_lib:RIKEN full-length enriched mouse cDNA library clone:7310032608.
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Methods Enzymol. 303, 19-44 (1999)
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High-efficiency full-length of
Mus musculus adult male ton
library, clone:2310032G08,
AK009571
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Committee the control of control of the control of control of the control of the control of contro Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL.http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Please visit our web site (http://genome.gsc.riken.go.jp/) for Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y Direct Submission

HTC

1349 bp

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us-09-333-159-47.p2n.rst

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  end: XhoI; 3'
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                                      FEATURES
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/db_xref="MGD:MGI:1914967"
/clone="2310047GI5"
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/db_xref="G1:12844939"
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Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDRA was primed with a primer [5' GGGAGGAGAAGGACCAAGAGCTTTTTTTTTTTVIN'] 1, cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. CDNA went through one round of normalization to Rot = 5.0 and subtraction to of sequence [5' and strand cDNA was prepared with the primer adapter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shibes)
Shibata,K. Itoh,M., Alzawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Shibata,K., Itoh,M., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Kikuchi,N., Ishil,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Rashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yondda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Okaza,E., Matsuura,S., Okaza,E., Matsuura,S., Okaza,E., Matsuura,S., Shikawa,M., Inoue,Y. and Hayashizaki,Y. Sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A., Arakawa,T., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanaqaki,T., Hara,A., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Hanaqaki,T., Hara,A., Hoya,M., Izawa,M., Kato,H., Kawai,J., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A.,
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                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                             Mus musculus (strain:C578L/6J) adult male tongue cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library
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Nature 409, 685-690 (2001)
5 (bases 1 to 1349)
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library, clone:2310047G15, full insert sequence
AK009875
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High-efficiency full-length cDNA cloning
Methods Enzymol. 303, 19-44 (1999)
                                                                      AK009875.1 GI:12844938
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2 (sites)
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itch,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)

20499374 3 (sites)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning Methods Enzymol. 303, 19-44 (1999)

mRNA,

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Mus musculus (strain:C57BL/6J) adult male tongue cDNA to clone_lib:RIKEN.full-length enriched mouse cDNA library

clcne:2310067K20

Mus musculus

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AK010093.1 GI:12845297

CAF trapper.

Shibate, Y. Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Kituchi, N., Ishine, T., Harama, M., Nishine, T., Harada, A., Yamamuco, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Okazaki, Y., Muramatsu, M., Inoue, Y. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format Genome Res. 10 (11), 1757-1771 (2000)

The RIKEN Genome Exploration Research Group Phase II Team and FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
5 (bases 1 to 1350)
Adachi, J., Alzawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A.

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                                       sSerAsnIleMetLeuLeuLeuGlyGlyPheAsnThrAsnAsnMetAsnM
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Adachi, J. Alzawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Haraqaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Hara, A., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Hara, A., Hayatsu, N., Hiramoto, K., Hiraoka, T., Marsyama, T., Miyazaki, A., Nibi, Y., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Miyazaki, A., Shibata, K., Saho, R., Sata, C., Sakai, C., Sakai, K., Shibata, K., Shibata, Y., Shinaqawa, A., Shiraki, T., Sacab, Y., Shibata, K., Shibata, Y., Takahashi, F., Tanaka, T., Teljma, Y., Toya, T., Yammura, T., Yasunishi, R., Socabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Shiraki, T., Socabe, Y., Suzuki, M., Muramatsu, M. and Hayashizaki, Y. Dolirect Submission Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), Riken Submission Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), Riken Genome Papicate visit our web site (http://genome.gsc.riken.go.jp, Tel:81-45-503-922, Tex:81-45-503-9216)

Please visit our web site (http://genome.gsc.riken.go.jp/) for CUN:http://genome Science Laboratory in Riken Genome Sciences Center and Genome Exploration Research of Genome Exploration Research of Toup in Riken Genome Science Laboratory in Riken Genome Science Laboratory in Riken Genome Sciences Center and Genome Science Laboratory in Riken Genome Sciences Center and Comme Science Laboratory in Riken Genome Science Genome Colence Genome Science Colence Center and Genome Science Laboratory in Riken Genome Science Co
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AK010093 1350 bp mRNA HTC 08-FEB-2001 Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310067K20, full insert sequence.

LOCUS

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319 aPheAspTrpGlySerGluThrLysAsnLeuGluLysCysAsnGlnProT 336
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723 TAITIGTAAAAAATGTICAIGCCCCACAACTACITAGAICAAITIGIT 772
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                                                                                                                                                                                                                                                                                                                                                                                                                   673
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                                                                                                                                                                                                                                                                                                                                  623
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pAlaGlyPheAspValTrpMetGlyAsnSerArgGlyAsnAlaTrpSerA 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 GTCCCAAAAACCCTGAAGCAAACATGATGTTAGTCAGATGATAACTTAC 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35 AGGCACTGG......CACTACAAGATGTGGCTGCTATTAGTAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               223 TCTGGGGGTCTATAGAATTCCTTATGGGAAGAAAAATTCTGAGAATATCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 lalaTyrMetPheGln...ArgasnValAsnSerValHisMetProThrL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39 ysAlaValAspProGluAlaPheMetAsnIleSerGluIleIleGlnHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GlnGlyTyrProCysGluGluTyrGluValAlaThrGluAspGlyTyrIl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.495
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US-09-333-159-47 x AK010093
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                     source
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ORIGIN
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                                                                                                                                                                                                                                                  CDS
  FEATURES
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205 622 672

269 813 863

319

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LOCUS AK010139 1350 bp mRNA HTC 08-FEB-2001
DEFINITION MUS musculus adult male tongue CDNA, RIKEN full-length enriched
11brary, clone:2310069P19, full insert sequence.
ACCESSION AK010139
                                                                                                                                                                                                                                                                                          1113
                                                                                                                                                                                                                                                                                                                                                                                                                              1163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1164 ACCTGGACTTCATCTGGGCGATGGATGCGCCTCAAGAGGTTTACAATGAG 1213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73 AAGIGIGCTATCTGCATTTGGAGGTGCACATGGCCTATTTGGAAAACTGG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           223 TCTGGGGGGTCTATAGAATTCCTTATGGGAAGAAAATTCTGAGAATATCG 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lySerArgProvalValLeuLeuGlnHisGlyLeuValGlyGlyAlaSer 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps: 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality: 1139.50
Ratio: 3.495
Hlatity: 79.319
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US-09-333-159-47 x AK010139
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Percent Similarity:
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         source
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ORIGIN
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L. Submitted (10-011-200) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemonic Sciences Center (GSC), Kanagawa 210-0045, Japan (E-mail:genome-reségscriken.go.jp, Rax:B1-45-503-9222, Pax:B1-45-503-9216)
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Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer 15' GAGAGAGAGAGACTOTTTTTTTTTTTTTTTVN 3'), CDNA was and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 5.0 and subtraction to sequence [5' second strand cDNA was prepared by using translation to Rot = 5.0 and subtraction to generate the primer adapter of sequence [5' second strand cDNA was prepared with the primer adapter.
                                                                                                                                                                                                                                                                                                                                                                                          Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNAs libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sibbta, K., Itch, M., Alzawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itch, M., Kikuchi, N., Ishila, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watshiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Okazaki, Y., Muramatsu, M., Inoue, Y. and Hayashizaki, Y. sequencing pipeline with 384 multicapillary sequencer Res. 10 (11), 1757-1771 (2000)
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Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                            Mus musculus (strain:C57BL/6J) adult male tongue cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library clone:2310069P19.
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Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
5 (bases 1 to 1350)
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Carifici,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)

High-efficiency full-length cDNA cloning Methods Enzymol. 303, 19-44 (1999)

(sites)

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Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.

Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; Carninci, P. and Hayashizaki, Y

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mRNA

clone_lib:RIKEN full-length enriched mouse cDNA to clone.lib:RIKEN full-length enriched mouse cDNA library clone:2310021B16.

Shibate, X. Itoh, M., Alzawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H.; Akiyama, J., Nishi, K.; Kitsunai, T., Tashiro, H., Itoh, M., Kituchi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegani, T., Kashiwagi, K., Fuliwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Okazaki, Y., Muramatsu, M., Inoue, Y. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format Genome Res. 10 (11), 1757-1771 (2000)

The RIKEN Genome Exploration Research Group Phase II Team and

FANTOM Consortium.

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            TyrAspGluMetAlaArgPheAspLeuProAlaValIleAsnPheIleLe 172
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Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakwa, T., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Aizawa, T., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hiranco, K., Hiraoka, T., Hori, F., Imotani, K., Ishil, Y., Itoh, M., Hiranco, K., Hiraoka, T., Hori, F., Moula, M., Koya, S., Kurihara, C., Matsuyama, T., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Kojima, Y., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Sakai, C., Sakai, C., Sakai, T., Sano, H., Sasaki, D., Shibata, Y., Shinaqawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yanamura, T., Yasunishi, A., Yoshina, Y., Toya, T., Yanamura, T., Yasunishi, A., Yoshina, M., Muramatsu, M. and Hayashizaki, Y. Direct Submission

AL Submitted (10-011-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKN), Laboratory for Genome Exploration Research Group, RIKEN Gemome, Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-reségsc.riken.go.jp, Physical Att. Sciences Cilken.go.jp, Physiol. 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 
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AK009431 1352 bp mRNA HTC 08-FEB-2001 Mus musculus adult male tongue cDNA, RIKEN full-length enriched 11brary, clone:2310021B16, full insert sequence. AK009431 GI:12844222

seq_documentation_block: LOCUS AK009431

DEFINITION ACCESSION VERSION

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCTGGGGGTCTATAGAATTCCTTATGGGAAGAAAATTCTGAGAATATCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps: 4
Percent Identity: 52.555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
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                                                                                                                                                                                                                                                                                                                                                                                    379
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                                                                                                                                                                                                                                                                                                                                                                                        σ
               /strain="C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from: 1
                                                                                                                                                                                                                                                                                                                                                                                    285
                                                                                                                                                                                   /note-"putative"
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                                                                                                                                                                                                                                                                                                                                                                                        O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality: 1139.50
Ratio: 3.495
Hlarity: 79.319
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                                                                                                                                                                                                                                                                                                                                                                                    291
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US-09-333-159-47 x AK009431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                    397
                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
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ORIGIN
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                                                                                                                                                                  CDS
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AK(09479 1343 bp mRNA HTC 08-FEB-2001 Mus musculus adult male tongue CDNA, RIKEN full-length enriched Ilbrary, clone:2310022K08, full insert sequence.
AK(09479.1 GI:12844303 CAP trapper.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1065
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         386
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                                                                                                                                          222
                                                                                                                                                                                                                                                                                    252
                                                                                                                                                                                                                                                                                                                                                        269
                                                                                                                                                                                                                                                                                                                                                                                                                              269 sSerAsnIleMetLeuLeuLeuGlyGlyPheAsnThrAsnAsnMetAsnM 286
                                                                                                       624
                                                                                                                                                                                                                                               724
                                                                                                                                                                                                                                                                                                                     774
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1116 TCCCAAACTCCCCAACCTTCTGTACCATAAGGAGATTCTTCCCTACAATC
                                                                                                                                                                                                                                    303 GlnAsnIleLeuHisTrpSerGlnAlaValAsnSerGlyGluLeuArgAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         369 uSerGluValThrAsnLeuIleTyrH1sLysAsnIleProGluTrpAlaH
 uGlnLysThrGlyGlnGluLysIleTyrTyrValGlyTyrSerGlnGlyT
                    hrThrMetGlyPheIleAlaPheSerThrMetProGluLeuAlaGlnLys
                                                                                      IleLysMetTyrPheAlaLeuAlaProIleAlaThrValLysHisAlaLy
                                                                                                                                                                             625 ATCAAGAGGTTTTATGCATTAGCTCCAGTTGCTACTGTGAAGTATACAGA
                                                                                                                                                                                                                sSerProGlyThrLysPheLeuLeuLeuProAspMetMetIleLysGlyL
                                                                                                                                                                                                                                                                                    euPheGlyLysLysGluPheLeu.....TyrGlnThrArgPheLeu
                                                                                                                                                                                                                                                                                                                   725 TATTIGGTAACAAATGTICATGCCCCACAACTACTTAGATCAATTICTT
                                                                                                                                                                                                                                                                                                                                                        253 ArgGlnLeuValIleTyrLeuCysGlyGlnValIleLeuAspGlnIleCy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ::|||||||| :::|||||||| 866 TGAGTCGATGTATCTAGGGCATAATCCAGGAACATCTACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       aPheAspTrpGlySerGluThrLysAsnLeuGluLysCysAsnGlnProT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hrProvalArgTyrArgValArgAspMetThrvalProThrAlaMetTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 386 isValAspPheIleTrpGlyLeuAspAlaProHisArgMetTyrAsnGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1216 ATAGTTACCATGATGGCAGAAGACTAACAGAAT 1248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: gb_ht.c:AK009479
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DEFINITION
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VERSION
KEYWORDS
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172
                                   525
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                                                                      189
                                                                                                                                                                                                              222
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ORGANISM

SOURCE

REFERENCE AUTHORS TITLE

JOURNAL REFERENCE AUTHORS JOURNAL

TITLE

MEDLINE REFERENCE AUTHORS

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GOEKIHYVGHSQGTTIGFIAFSTNPALAKKIKRFYALAPVATVKYTESPFKKISLIPK
ELKVIEROKKHEMPHNYLDQFLGTEVCSRELLDLCSNALFFRGGEDSKNLNVSRFDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122 pAlaGlyPheAspValTrpMetGlyAsnSerArgGlyAsnAlaTrpSerA 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89 lySerArgProValValLeuLeuGlnHisGlyLeuValGlyGlyAlaSer 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   106 AsnTrpIleSerAsnLeuProAsnAsnSerLeuGlyPheIleLeuAlaAs 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        139 rgLysHisLysThrLeuSerIleAspGlnAspGluPheTrpAlaPheSer 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           420 GGAAAAATGTATACTATTCACCAGACTCAGTTGAATTCTGGGCTTTCAGC 469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56 GlnGlyTyrProCysGluGluTyrGluValAlaThrGluAspGlyTyrIl 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72 eLeuSerValAsnArgIleProArgGlyLeuValGlnProLysLysThrG 89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 ArgGlnTrpIleValSerHisArgMetGluMetTrpLeuLeuIleLeuVa 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       320 AACTGGATTACAAATCTGCCAAACAACAGCCTGGCCTTCATTCTAGCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32 AGGCACTGG......CACTACAAGATGTGGCTGCTATTAGTAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39 ysalavalaspproglualaPhemetAsnIleSerGluIleIleGlnHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Identity: 52.555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                378 t
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                                                                                           /db_xref="MGD:MGI:1896992"
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50. .1237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
                                                                                                                                                                                                                                              /sex="male"
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US-09-333-159-47 x AK009479
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Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA, was primed with a primer 15' AGGAGAGAGAAGGATTTTTTTTTTTTTVN 3'), cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went truculy one round of normalization to Rot = 5.0 and subtraction to of sequence 15'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shibata, K., Itoh, M., Alzawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H.; Itoh, M., Kitsunai, T., Tashiro, H.; Itoh, M., Nishine, T., Nakamura, S., Hazama, M., Nishine, T., Itada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunra, S., Okazaki, Y., Muramatsu, M., Inoue, Y. and Hayashizaki, Y. Sequencing pipeline with 384 multicapillary sequencer Cennat Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Sushiro-cho, Tsurumi-ku, Yokohama, Ranagawa 230-0045, Japan (E-mail:genome-reségsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-922, Fax:81-45-503-9216)
Please visit our web site (http://genome.gsc.riken.go.jp/) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cleaved
                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (strain:C57BL/6J) adult male tongue cDNA to mRNA, clone_11b:RIKEN full-length enriched mouse cDNA library clone:2310022K08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             he RIKEN Genome Exploration Research Group Phase II Team and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unctional annotation of a full-length mouse cDNA collection tature 409, 685-690 (2001) (bases 1 to 1343)
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                                                                                                                                                                                                                                                                                                                                                                 High-efficiency full-length cDNA cloning
Methods Enzymol. 303, 19-44 (1999)
                                                                                                                                                                                                                                                                                                                        Carninci, P. and Hayashizaki, Y.
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MEDLINE REFERENCE AUTHORS

JOURNAL

TITLE

TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL

COMMENT

156 TyrAspGluMetAlaArgPheAspLeuProAlaValIleAsnPheIleLe 172

/organism-"Mus musculus"

source

FEATURES

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clone:2310022H17.
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                              Mus musculus
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Shibata, K.,
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CAP trapper.
Mus musculus (strain:C578L/6J) adult male tongue CDNA
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               519
                                                                                                                            253 ArgGlnLeuValIleTyrLeuCysGlyGlnValIleLeuAspGlnIleCy 269
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                                                                                                           hrThrMetGlyPheIleAlaPheSerThrMetProGluLeuAlaGlnLys 205
                                                                                                                                                                          206 IleLysMetTyrPheAlaLeuAlaProIleAlaThrValLysHisAlaLy 222
                                                                                                                                                                                                                                          222 sSerProGlyThrLysPheLeuLeuLeuProAspMetMetIleLysGlyL 239
                                                                                                                                                                                                                                                            sSerAsnIleMetLeuLeuLeuGlyGlyPheAsnThrAsnAsnMetAsnM 286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     286 etSerArgAlaSerValTyrAlaAlaH1sThrLeuAlaGlyThrSerVal 302
172 uGlnLysThrGlyGlnGluLysIleTyrTyrValGlyTyrSerGlnGlyT
                                                                           520 ACAGAAAACTGGACAAGAGAAAATACACTATGTTGGTCACTCTCAGGGCA
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KEYWORDS
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L Value 409, 685-690 (2001)

E 5 (bases 1 to 1345)

S Adachi, J., Alzawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A.,
Arakwa, T., Carninci, P., Fukuda, S., Fukunish, Y., Furuno, M.,
Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F.,
Imotani, K., Ishli, Y., Itoh, M., Izawa, M., Kato, H., Kwami, J.,
Kojima, Y., Konno, H., Kouda, M., Kato, K., Matsujama, T.,
Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y.,
Okido, T., Owa, C., Saito, H., Saito, R., Sakai, K., Sano, H.,
Sasaki, D., Shibata, K., Shibata, Y., Shinaqawa, A., Shiraki, T.,
Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,
Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A.,
Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
Direct Submission

L Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
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Please visit our web site (http://genome.gsc.riken.go.jp/) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carnincl,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Kituchi,N., Ishilo,T., Nakamura,S., Hazama,M., Nishine,T., Harda,A., Yamancio,R., Matsumoto,H., Sakayuchi,S., Ishinayi,K., Fujiwake,N., Matsumoto,H., Sakayuchi,S., Isawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Okazaki,Y., Muramatsu,M., Inoue,Y. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The RIKEN Genome Exploration Research Group Phase II Team and
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clone_lib:RIKEN full-length enriched mouse cDNA library
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High-efficiency full-length cDNA cloning
Methods Enzymol. 303, 19-44. (1999)
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172 TITGATGAAATGGCTAAATATGACCTTCCAGCCACCATAGACTTCATTGT
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Ratio: 3.492
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mRNA HTC 08-FEB-2001 tongue cDNA, RIKEN full-length enriched
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CAP trapper.
Mus musculus (strain:CS7BL/6J) adult male tongue cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library
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                                                                                                                                                                                                                                                  sSerProGlyThrLysPheLeuLeuLeuProAspMetMetIleLysGlyL 239
                                                                                                                                                                                                                                                                                         721
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                                       571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GlnAsmileLeuHisTrpSerGlnAlaValAsmSerGlyGluLeuArgAl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  353 ThrGlyGlyGlnAspTrpLeuSerAsnProGluAspValLysMetLeuLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1113 TCCCANACTCCCCAACCTTCTGTACCATAAGGAGATTCTTCCCTACAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        isValAspPheIleTrpGlyLeuAspAlaProHisArgMetTyrAsnGlu
                                                                                                                                                                                     .....TGCTCACGGAGCTGCTAGATCTTCTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ::||||||| :::|||||||| 863 IGAGTCGCTTTGATGTATCTAGGGCATAATCCAGGAAGAACATGTACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11brary, clone:2310028109, full insert sequence AK009523
                                                                                                                                                                                                                                                                                                                                                             aPheAspTrpGlySerGluThrLysAsnLeuGluLysCysAsnGlnProT
uGlnLysThrGlyGlnGluLysIleTyrTyrValGlyTyrSerGlnGlyT
                          hrThrMetGlyPheIleAlaPheSerThrMetProGluLeuAlaGlnLys
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                                                                                                                                                               206 IleLysMetTyrPheAlaLeuAlaProIleAlaThrValLysHisAlaLy
                                                                                                                                                                                                                                                                                         672 AAGTCCCTTTAAAAAGATTTCACTTATTCCTAAGTTTCTTCTCCAAGGTGA
                                                                                                                                                                                                                                                                                                                                     euPheClyLysLysGluPheLeu.....TyrGlnThrArgPheLeu
                                                                                                                                                                                                                                                                                                                                                                                                                        253 ArgGlnLeuValIleTyrLeuCysGlyGlnValIleLeuAspGlnIleCy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1213 ATAGTWACCATGATGGCAGAAGACTAACAGAAT 1245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         403 IleIleHisLeuMetGlnGlnGluGluThrAsn 413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       273 GCAAGAGACCTGTGGCATATTTGCAGCATGGTTTGATTGCATCAGCCACA 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56 GlnGlyTyrProCysGluGluTyrGluValAlaThrGluAspGlyTyrIl 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ......CACTACAAGATGTGGCTGCTATTAGTAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     173 TGGGGATATCCAAGTGAGGAATATGAAGTTGTTACTGAAGATGGCTACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          223 TCTGGGGGTCTATAGAATTCCTTATGGGAAGAAAATTCTGAGAATATCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 ArgGlnTrplleValSerHisArgMetGluMetTrpLeuLeuIleLeuVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23 lAlaTyrMetPheGln...ArgAsnValAsnSerValHisMetProThrL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39 ysAlaValAspProGluAlaPheMetAsnIleSerGluIleIleGlnHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72 eLeuSerValAsnArgIleProArgGlyLeuValGlnProLysLysThrG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               139 rgLysHisLysThrLeuSerIleAspGlnAspGluPheTrpAlaPheSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Identity: 52.555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from: 1 to: 1346
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53. .1240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  283 g
                                                                                                                                                                                                                                               /note="putative"
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                                                                                              /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            289 c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNAs libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shibate, X. Itoh, M., Alzawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Kitsunai, T., Tashiro, H., Itoh, M., Yahunchi, N., Ishine, T., Yamamoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunra, S., Okazaki, Y., Muramatsu, M., Inoue, Y. and Hayashizaki, Y. SIKIR integrated sequence analysis (RISA) system-384-format Genome Res. 10 (11), 1757-1771 (2000)
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                                                           Chordata, Craniata, Vertebrata, Euteleostomi,
Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The RIKEN Genome Exploration Research Group Phase II Team and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5 (bases 1 to 1346)
                                                                                                                                                Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Methods Enzymol. 303, 19-44 (1999)
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                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FANTOM Consortium.
clone:2310028109
                               Mus musculus
                                                                                                                       (sites)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (sites)
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                            ORGANISM
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TITLE
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MEDLINE
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473 TTTGATGAAATGGCTAAATATGACCTTCCAGCCACCATCGATGATTGT 522

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/organism="Mus musculus" /strain="C57BL/6J" /db_xref="taxon:10090"

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Mus musculus adult male tongue CDNA, RIKEN full-length enriched library, clone:2310040L03, full insert sequence.
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Mus musculus (strain:C57BL/6J) adult male tongue CDNA to
clone_lib:RIKEN full-length enriched mouse cDNA library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   964 CTATAACTGGGGAAGTCCATTACAGAACATGTTACACTACAATCAGAAAA 1013
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        336 hrProvalArgTyrArgValArgAspMetThrValProThrAlaMetTrp 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          353 ThrGlyGlyGlnAspTrpLeuSerAsnProGluAspValLySMetLeuLe 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          369 uSerGluValThrAsnLeuIleTyrHisLysAsnIleProGluTrpAlaH 386
205
                                                                                             623 ATCAAGAGGTTTTATGCATTAGCTCCAGTTGCTACTGTGAAGTATACAGA 672
                                                                                                                                                                                                                                                                                                                                                               239 euPheGlyLysLysGluPheLeu......TyrGlnThrArgPheLeu 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               etSerArgAlaSerValTyrAlaAlaHisThrLeuAlaGlyThrSerVal 302
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                                                                                                                                                                    206 IleLysMetTyrPheAlaLeuAlaProIleAlaThrValLysHisAlaLy 222
                                                                                                                                                                                                                                                                    222 sSerProGlyThrLysPheLeuLeuLeuProAspMetMetIleLysGlyL 239
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                                                                      hrThrMetGlyPheIleAlaPheSerThrMetProGluLeuAlaGlnLys
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Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itch,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Adachl, J., Alzawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hangagki, T., Hara, H., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Ishii, Y., Ishii, Y., Ishii, Y., Ishii, Y., Kouda, M., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Oka, C., Salto, H., Saito, H., Saito, H., Sakai, K., Sano, H., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, PRI:http://genome-gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                         Shibate, X. Itoh, M., Alzawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Kitsunai, T., Tashiro, H., Itoh, M., Tishi, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohra, E., Watshiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Okazaki, Y., Muramatsu, M., Inoue, Y. and Hayashizaki, Y. RIKEN Integrated sequence analysis (RISA) system--384-format Sequencing pipeline with 384 multicapillary sequencer
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Disect Submission
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
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The RIKEN Genome Exploration Research Group Phase II Team and
FANTOM Consortium.
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Nature 409, 685-690 (2001)
5 (bases 1 to 1346)
                                                                                                         Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Methods Enzymol. 303, 19-44 (1999)
                                                                                                                                                                                                                                                                                                                                           Res. 10 (10), 1617-1630 (2000)
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Shibata, K.,
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AND MUS MUSCULUS AGUIT MAIR EDNA, RIKEN full-length enriched library, clone:2310068005, full insert sequence.

AK010116
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Mus musculus (strain:C57BL/6J) adult male tongue cDNA to mRNA,
clone_llb:RIKEN full-length enriched mouse cDNA library
clone:2310068005.

Mus musculus
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 sSerProGlyThrLysPheLeuLeuLeuProAspMetMetIleLysGlyL
                                                                                                                                                                                                                                                                             euPheGlyLysLysGluPheLeu......TyrGlnThrArgPheLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  isValAspPhelleTrpGlyLeuAspAlaProHisArgMetTyrAsnGlu
                                                                     hrThrMetGlyPheIleAlaPheSerThrMetProGluLeuAlaGlnLys
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AK010116,1 GI:12845334
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TTTGATGAATGGCTAAATATGACCTTCCAGCCACCATAGACTTCATTGT 522
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Percent Identity: 52,555
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Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' AGAGAGAGAAGACTOTTTTTTTTTTTTTVN 3'), CDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 5.0 and subtraction to General Science [5' and strand cDNA was prepared with the primer adapter of sequence [5' and strand cDNA was prepared with the primer adapter.
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                                                                                                                                                                                                                           Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA: libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Nature 409, 685-690 (2001)
(bases 1 to 1347)
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URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
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                                                                                                 Carninci,p. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Methods Enzymol. 303, 19-44 (1999)
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COMMENT

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FILADAGYDVWLGNSRGNTWSRKNVYYSPDSVEFWAFSFDEMAKYDLPATIDFIVQKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71 AAGTGIGCTATCTGCATTTGGAGGIGCACATGGCCTATTTGGAAAACTGG 120
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                                                                                                                 /note-"putative"
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CDNA library was prepared and sequenced in Mouse Genome Enroyative Training the Concession of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer 15' AGGAGAGAGAGGAGGACTITITITITITITIVIN'3'), cDNA was and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 5.0 and subtraction to of sequence [5' Second strand cDNA was prepared with the primer adapter of sequence [5' Second strand cDNA was prepared with the primer adapter of sequence [5').
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Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
Konno,H., Aiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
Kikuchi,N., Ishili,Y., Nakamura,S., Hazama,M., Nishino,T.,
Harada,A., Yamamoto,R., Matsumoto,H., Sakaquchi,S., Ikegami,T.,
Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watshiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
RIKEN integrated sequence analysis (RISA) system--384-format
Sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
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     Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Direct Submission
                                                        Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Methods Enzymol, 303,.19-44 (1999)
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5 (bases 1 to 1348)
Adachi,J., Alzawa,K., Akahi
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Mus musculus-(strain:C57BL/6J) adult male tongue cDNA to mRNA,
clone_lib:RIKEN full-length enriched mouse cDNA library
clone:2310066C03.

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Mus musculus adult male tongue CDNA, RIKEN full-length enriched
library, clone:2310066C03, full insert sequence.
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303 GlnAsnIleLeuHisTrpSerGlnAlaValAsnSerGlyGluLeuArgAl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 ArgGlnTrpIleValSerHisArgMetGluMetTrpLeuLeuIleLeuVa 23
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Identity: 52.555
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US-09-333-159-47 x AK010058
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Percent Similarity:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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LOCUS AK009300 1349 bp mRNA HTC 08-FEB-2001
DEFINITION Mus musculus adult male tongue cDNA, RIKEN full-length enriched
1 library, clone:2310011G18, full insert sequence.
ACCESSION AK009300
VERSION AK009300.1 GI:12844011
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Mus musculus (strain:C57BL/6J) adult male tongue CDNA to mRNA, clone_lib:RIKEN full-length enriched mouse CDNA library clone:2310011G18.
Mus musculus
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                      206 IleLysMetTyrPheAlaLeuAlaProIleAlaThrValLysHisAlaLy
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TATTTGiTAACAAAATGTTCATGCCCCACAACTACTTAGATCAATTTCTT
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                                                full-length enriched mouse cDNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73 AAGTGTGCTATCTGCATTTGGAGGTGCACATGGCCTATTTGGAAAACTGG 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23 lAlaTyrMetPheGln...ArgAsnValAsnSerValHisMetProThrL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ysAlaValAspProGluAlaPheMetAsnIleSerGluIleIleGlnHis
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                                                                                                         CDS
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                                                                                                                                                Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Adachli, Alzawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakwa, T., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatu, N., Hiramoto, K., Hiracoka, T., Hori, F., Imotani, K., Ishii, Y., Icoh, M., Izawa, M., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Sato, H., Salto, H., Salto, H., Salto, H., Salto, H., Salto, R., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Tagawa, A., Takahashi, F., Tanaka, T., Yeshino, M., Muramata, H., Yasunishi, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y., Direct Submission
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Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' AGGAGAGAGAGAGCTTTTTTTTTTTTTVN 3', CDNA was prepared by using trebalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went trough one round of normalization to Rot = 5.0 and subtraction to essence [5' escond strand cDNA was prepared with the primer adapter of sequence [5' escond strand cDNA was prepared with the primer adapter.
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Nature 409, 685-690 (2001)
5 (bases 1 to 1349)
      1 (sites)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Methods Enzymol. 303, 19-44 (1999)
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Functional annotation of a full-length mouse cDNA collection

In Nature 409, 685-690 (2001)

E 5 (bases 1 to 1349)

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Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A.,

Arakawa, T., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M.,

Hanngaki, T., Hara, A., Hayatau, N., Hiramcto, K., Hiraoka, T., Hori, F.,

Imotani, K., Ishil, Y., Itoh, M., Itawa, M., Kato, H., Kawai, J.,

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Kojima, Y., Konno, H., Rouda, M., Koya, S., Kurihara, C., Matsuyama, T.,

Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H.,

Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Sakai, K., Sano, H.,

Sogube, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,

Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A.,

Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.,

Direct Submission
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Shizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Kikuchi, N. Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M.,
Kikuchi, N. Ishii, Y., Nakamura, S., Hazama, M., Nishine, T.,
Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T.,
Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
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RIKEN integrated sequence analysis (RISA) system-184-format
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Second strand cDNA was prepared with the primer adapted
                                                                                           Cardinci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length CDNA libraries for rapid discovery of new Genome Res. 10 (10), 1617-1630 (2000)
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The RIKEN Genome Exploration Research Group Phase II Team and
FANROM Consortium.
                          full-length cDNA cloning
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                      sSerAsnIleMetLeuLeuLeuGlyGlyPheAsnThrAsnAsnMetAsnM 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       etSerArgAlaSerValTyrAlaAlaHisThrLeuAlaGlyThrSerVal 302
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                                                 GGTACGGAAGTG......TGCTCACGGGAGCTGCTAGATCTTCTCTG
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                          hrThrMetGlyPheIleAlaPheSerThrMetProGluLeuAlaGlnLys
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                                                                                                                                                                                                                                                                                                                                                                                                                         253 ArgGlnLeuValIleTyrLeuCysGlyGlnValIleLeuAspGlnIleCy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       369 uSerGluValThrAsnLeuIleTyrHisLysAsnIleProGluTrpAlaH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             isValAspPheIleTrpGlyLeuAspAlaProHisArgMetTyrAsnGlu
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hrThrMetGlyPheIleAlaPheSerThrMetProGluLeuAlaGlnLys
                   Carrinci, P. and Hayashizaki, Y
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VERSION
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   cDNA library'
   enriched mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35 AGGCACTGG......CACTACAAGATGTGGCTGCTATTAGTAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             106 AsnTrplleSerAsnLeuProAsnAsnSerLeuGlyPheIleLeuAlaAs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72 eLeuSerValAsnArgIleProArgGlyLeuValGlnProLysLysThrG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   223 TCTGGGGGTCTATAGAATTCCTTATGGGAAGAAAATTCTGAGAATATCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 156 TyrAspGluMetAlaArgPheAspLeuProAlaValIleAsnPheIleLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length: 411
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Percent Identity: 52.555
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US-09-333-159-47 x AK009474
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                              CDS
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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LOCUS AK009546 1349 bp mRNA HTC 08-FEB-2001

DEFINITION MUS musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310030L19, full insert sequence.

ACCESSION AK009546

VERSION AK009546.1 GI:12844406
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Mus musculus (strain:C57BL/6J) adult male tongue CDNA to clore_11b:RIKEN full-length enriched mouse CDNA library close:2310030L19.
Mus musculus
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                                                                                                                                                                                                                                                                                                             GGTACGGAAGTG......TGCTCACGGAGCTGCTAGATCTTCTCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                    814 CAGCAACGCTTTATTCATCTTCTGTGGATTTGACAAGAAAACTTAAATG
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                                                                                                                                                                                    euPheGlyLysLysGluPheLeu......TyrGlnThrArgPheLeu
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|| | ATAGTTACCATGGCAGAAGACTAACAGAAT |||
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76 AAGTGTGCTATCTGCATTTGGAGGTGCACATGGCCTATTTGGAAAACTGG 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89 lySerargProValValLeuLeuGlnHisGlyLeuValGlyGlyAlaSer 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 156 TyrAspGluMetAlaArgPheAspLeuProAlaValIleAsnPheIleLe 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  172 uGlnLysThrGlyGlnGluLysIleTyrTyrValGlyTyrSerGlnGlyT 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      189 hrThrMetGlyPheIleAlaPheSerThrMetProGluLeuAlaGlnLys 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56 GlnGlyTyrProCysGluGluTyrGluValAlaThrGluAspGlyTyrIl 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38 AGCCACTGG......CACTACAAGATGTGGCTGCTATTAGTAAC 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72 eLeuSerValAsnArgIleProArgGlyLeuValGlnProLysLysThrG
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Ratio: 3.492
Percent Similarity: 79.319
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US-09-333-159-47 x AK009546
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                                      CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGIN
                                                                                                                                                                                                                                                                                                                          Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Shuchi, N., Ishili, Y., Nakamura, S., Hazama, M., Nishine, T., Tanada, A., Yamamoto, H. Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Okazaki, Y., Muramatsu, M., Inoue, Y. and Hayashizaki, Y. Sequencing pipeline with 384 multicapillary sequencer General Conneces. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Adachiji, Aizawa K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, Hayatau, N., Hiramoto, K., Hiraoka, T., Hori, F., Imotani, K., Ishli, Y., Itoh, M., Izawa, M., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohoo, M., Okazaki, Y., Oka, C., Satto, H., Saito, R., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yammura, T., Yasunishi, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5, GAGAGAGAGATCCAAGAGCTCTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 5.0 and subtraction to Rot = 25.0. Second strand cDNA was prepared with the primer adapter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="tongue" /close_lib="RIKEN full-length enriched mouse cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research (SIKEN), Laboratory for Genome Exploration Research (SIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Ranagawa 230-0045, Japan (E-mail:genome-reségsc.riken.go.jp, URL.http://genome-gsc.riken.go.jp/, Tel:81-45-503-9212,
                                                                                                                                                                                                             new genes
                                                                                              Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected conns to prepare full-length con A. Ibraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Please visit our web site (http://genome.gsc.riken.go.jp/) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The RIKEN Genome Exploration Research Group Phase II Team and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
   High-efficiency full-length cDNA cloning
Methods Enzymol. 303, 19-44 (1999)
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/db_xref="taxon:10090"
/db_xref="MGD:MGI:1893997"
/db_xref="MGD:HGI:1914967"
/clone="2310030L19"

    11349
/organism="Mus musculus"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FANTOM Consortium.
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1067 AACGGTGGCCATGACATCCTGGCTGATCCCCAAGATGTCGCAATGCTGCT 1116
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222 sSerProGlyThrLysPheLeuLeuLeuProAspMetMetIleLysGlyL 239
                                                                                                                                               euPheGlyLysLysGluPheLeu......TyrGlnThrArgPheLeu 252
                                                                                                                                                                                                                                   775
                                                                                                                                                                                                                                                                    253 ArgGlnLeuValIleTyrLeuCysGlyGlnValIleLeuAspGlnIleCy 269
                                                                                                                                                                                                                                                                                            sSerAsnIleMetLeuLeuLeuGlyGlyPheAsnThrAsnAsnMetAsnM 286
                                                                                                                                                                                                                                                                                                                                                             etSerArgAlaSerValTyrAlaAlaHisThrLeuAlaGlyThrSerVal 302
                                                                                                                                                                                                                                                                                                                                                                                                                                  303 GlnAsnIleLeuHisTrpSerGlnAlaValAsnSerGlyGluLeuArgAl 319
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                                                     206 IleLysMetTyrPheAlaLeuAlaProIleAlaThrValLysHisAlaLy
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TATITGGTAACAAAATGTTCATGCCCCACAACTACTTAGATCAATTTCTT
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82.50 122.45 33.26
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82.50 109.43 176.52
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82.50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37 ProThrLy3AlaValAspProGluAlaPheMetAsnIleSerGluIleIl
                                                                                                                                                                                                                  /cgn2_6/ptodata/1/ina/5A_COMB.seq:US-08-227-108-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Junien, Jean-Louis
TITLE OF INVENTION: Recombinant Dog Gastric Lipase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps: 3
Percent Identity: 56.452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: US-08-227-108-2 from: 1 to: 1137
   /cgn2_6/ptodata/l/ina/SB_COMB.seq:US-08-600-908A-11 + /cgn2_6/ptodata/l/ina/6A_COMB.seq:US-08-683-838A-11 + /cgn2_6/ptodata/l/ina/SB_COMB.seq:US-08-483-101-1 + /cgn2_6/ptodata/l/ina/SA_COMB.seq:US-08-483-101-1 + /cgn2_6/ptodata/l/ina/SA_COMB.seq:US-08-905-817-1 + 1
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1355 Avenue of the Americas
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                                                                                                                                                                                                                                                                 seq_documentation.block:
    Sequence 2, Application US/08227108
    Patent-No: 5807726
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US-09-333-159-47 x US-08-227-108-2
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COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30,256
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TELEPHONE: 212 790-9090
TELEFAX: 312 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Blanchard, Claire APPLICANT: Benicourt, Claude
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 03-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Fanucci, Allan A. REGISTRATION NUMBER: 30, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGIH: 1:137 base pairs
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality: 1141.50
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Percent Similarity: 84.677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SECUENCES: 2. CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: New York
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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STREET: 13
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; LOCATION:
US-08-227-108-2
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1167 | 2521 | 2526 | 46899 | 2160 | 2160 | 40328 | 6027 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 | 2160 
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92.00 153.99 0.5820
92.00 153.96 0.8839
92.00 116.26 73.51
91.00 153.79 0.5967
91.00 153.79 0.5967
91.00 116.02 75.82
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1.7e-129
2.8e-129
2.8e-129
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                                                                                                                                             About: Results were produced by the GenCore software, version 4.5. Copyright (c) 1993-2000 Compugen Ltd.
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1007 TITCCAAGCTCCCCAATCTCATTTACCACGGAAGAITCCTCCTTACAAT 1056 386 HisvalaspenerierrpGlyLeuAspalabroHisArgMerryrAsnGl 402 Seq_name: /cgn2_6/ptodata/1/ina/5B_cOWB.8eq:US-09-073-674-2 GENERAL INFORMATION:
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BARDADATION:
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APPLICANT:
AUTLE OF INVENTED:
AUTLE OF SEQUENCE, 2
AUDRESCEE:
AUDRESCEE:
AUTHORITION:
STREET: 2800 | Warder-Lambert Company ZIP: 48105.3.n.
ZIP: 48105.3.n.
COMPUTER READABLE FORM:
COMPUTER IBM PC COMPALISE
COMPUTER IBM PC COMPALISE
SOFTWARE: PACEDIS MS-DOS
CURRENT APPLICATION NELEASE #1.0, Version #1.25
FITTING NAMER: US/09/073,674 Seq.documentation_block; Sequence 2, Application US/09073674; Patent No. 5998189; GENERAL INFORMATION: 1107 AATTGTTTCCATGATG 1122 REFERENCE/DOCKET NUMBER: 507
TELECOMMINICATION INFORMATION:
TELEPANE: 734 622-7530
TELEPANE: 734 622-7530 ATORNEY AGENT INFORMATION:
NAME: Crissey, Todd M.
REGISTRATION NUMBER: 37, F INFORMATION FOR SEQ ID NO: 2: LENGTH: 1137 base Pairs STRANDEDNESS: double MOLECULE TYPE: CDNA to MRNA Ouality: 1141.50 1..1137 NAME/KEY: LOCATION: US-09-073-674-2 alignment_scores;

957 GAACGGTGGCAACGACTTGCTGGCCGACCTCACGATGTTGACCTTTTGC 1006 Align seg 1/1 to: US-09-073-674-2 from: 1 to: 1137

Gaps:

Gaps:
3
36.452

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GluPheTrpAlaPheSerTyrAspGluMetAlaArgPheAspLeuProAl 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            856
                                                                                                                  :::III ||||||::: ::: ::: :::::::!||
                                                                                                                                                                                                                                                                                                 LeuValGlyGlyAlaSerAsnTrpIleSerAsnLeuProAsnAsnSerLe 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rgGlyAsnAlaTrpSerArgLysHisLysThrLeuSerIleAspGlnAsp 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAATICIGGGCTITCAGITATGATGAGATGGCAAAATATGACCTACCAGC 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aValIleAsnPheIleLeuGlnLysThrGlyGlnGluLysIleTyrTyrV 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alGlyTyrSerGlnGlyThrThrMetGlyPheIleAlaPheSerThrMet 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProGluLeuAlaGlnLysIleLysMetTyrPheAlaLeuAlaProIleAl 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aThrValLysHisAlaLysSerProGlyThrLysPheLeuLeuProA 233
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                                                                                                                                                                                                                                                 LeuGluThrLeuSerArgGlnTrpIleValSerHisArgMetGluMetTr 18
                                                                                                                                                           18 pLeuLeuIleLeuValAlaTyrMetPheGlnArgAsnValAsnSerValH 35
                                                                                                                                                                                                                   35 isMetProThrLys.....AlaValAspProGluAlaPheMetAsnIle 49
                                                                                                                                                                                                                                                                              SerGlullelleGlnHisGlnGlyTyrProCysGluGluTyrGluValAl 66
                                                                                                                                                                                                                                                                                                                                       aThrGluAspGlyTyrIleLeuSerValAsnArgIleProArgGlyLeuV 83
                                                                                                                                                                                                                                                                                                                                                                                                alGlnProLysLysThrGlySerArgProValValLeuLeuGlnHisGly 99
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 Percent Identity: 60.732
                                                                         to: 2626
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Bukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (basis: 1 to 2493)
Anderson, R.A. and Sando, G.N. Cloning and expression of cDNA encoding human lysosomal acid lipase/cholesteryl ester hydrolase. Similarities to gastric and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_b)pck:
LOCUS HUMLIPCML 2493 bp mRNA
DEFINITION HUMEN 1/90somal acid lipase/cholesteryl esterase mRNA, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="alternate initiator ATG may be at position 47'
1156
                                                                                                                                                                                                                                                                                                                     /codon_start=1
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                                                                      300 ThrSerValGLnAsnIleLeuHisTrpSerGlnAlaValAsnSerGlyGl
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                                                                                                                                                                                                                                                                                                   350 AlaMetTrpThrGlyGlyGlnAspTrpLeuSerAsnProGluAspValLy
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7. Biol. Chem. 266 (33), 22479-22484 (1991)
97. 0042193
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Homo sapiens fibroblast cDNA to mRNA.
Homo sapiens
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1. 2493
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VERSION
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AUTHORS
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/EC_number="3.1.1.13"
/note="alternate initiator ATG may
/codon_start=1
/db_xref="GDB:GOO-120-153"

/Product "1ysosomal acid)

Tue

/db_xref="G1:187152"
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NKTGGEQVYYVGHSGGTTIGFIAFSQIPETAKRIKKFFALGPVASVAFCTSPMAKLGR
LEPHLIKDLEFGDKEFLQPSAFLKWLGTHVCTHYILELGGGNTLGFGREBRILNMSR
VDYYTTHSPAGTSVQNMLHWSQDAVKFOKFQAFDWGSSARNYFHYNGSYPPTYNKDML
VPTAVWSGGHDWLADVYDVNILLTQITNLVFHESIPEWEHLDFIWGLDAPWRLYNKIL 47; /note="alternate signal peptide may begin at position 47 as predicted from von Heijne, G. (1986) Nucl. Acids Res 14,4683-4690; G00-120-153" esterase" /EC_number="3.1.1.13" /note="G00-120-153" /product="lysosomal acid lipase/cholesteryl 251 301 49 83 66 35 99 51 35 isMetProThrLys.....AlaValAspProGluAlaPheMetAsnIle 50 SerGluIleIleGlnHisGlnGlyTyrProCysGluGluTyrGluValAl 202 GACAGAAGATGGATATATTCTGTGCCTTAACCGAATTCCTCATGGGAGGA 2 LeuGluThrLeuSerArgGlnTrplleValSerHisArgMetGluMetTr .18 pLeuLeulleLeuValAlaTyrMetPheGlnArgAsnValAsnSerValH 66 aThrGluAspGlyTyrIleLeuSerValAsnArgIleProArgGlyLeuV alGlnProLysLysThrGlySerArgProValValLeuLeuGlnHisGly Length: 410 Gaps: 2 Percent Identity: 60.732 to: 2493 801 /note="G00-120-153" 2493 /gene="LIPA" /note="G00-120-153" a 484 c 516 g from: 1 41. .103 /gene="LIPA" 104. .1237 /gene="LIPA" 2466. .2471 / /gene="LIPA" Align seg 1/1 to: HUMLIPCHL US-09-333-159-47 x HUMLIPCHL Quality: 1306.00 Ratio: 3.841 Percent Similarity: 82.927 NLMRKYO' 692 polyA_signal alignment_scores: sig_peptide mat_peptide polyA_site alignment_block BASE COUNT ORIGIN 83

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133

17-FEB-1997 seq_documentation_block:
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HSIXACLY
LOCUS
HSIXACLY
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ACCESSION 231690
VERSION 231690.1 GI:506430